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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 09:00:24 ; Search time 2617 Seconds
(without alignments)
370.311 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcattgcacatcccatcttc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2104966

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

Database :

GenBnd1:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	65.0	54	6	AR356488 Sequence
C 2	13	65.0	54	6	AR538044 Sequence
C 3	13	65.0	60	6	COS48380 Sequence
C 4	12	60.0	20	6	AX293633 Sequence
C 5	12	60.0	21	6	AR148756 Sequence
C 6	12	60.0	24	6	AX289000 Sequence
C 7	12	60.0	26	6	AX551638 Sequence
C 8	12	60.0	26	6	AX703273 Sequence
C 9	12	60.0	29	6	AR039144 Sequence
C 10	12	60.0	29	6	AR065274 Sequence
C 11	12	60.0	29	6	BD061658 Sequence
C 12	12	60.0	39	6	AR128133 Sequence
C 13	12	60.0	51	6	AX116213 Sequence
C 14	12	60.0	51	6	AX159371 Sequence
C 15	12	60.0	51	6	AX159372 Sequence
C 16	12	60.0	51	6	AX159373 Sequence
C 17	12	60.0	51	6	AX165283 Sequence
C 18	12	60.0	55	11	HOMUT5280A
C 19	12	60.0	60	6	COS45434 Sequence

20	12	60.0	60	6	COS47633 Sequence
21	12	60.0	66	9	AY139609 Homo sapi
22	11	55.0	17	6	AR040149 Sequence
C 23	11	55.0	18	6	AR241626 Sequence
C 24	11	55.0	18	6	AR258715 Sequence
C 25	11	55.0	18	6	AX137953 Sequence
C 26	11	55.0	18	6	BD015843 DNA encod
C 27	11	55.0	19	6	AR174747 Sequence
C 28	11	55.0	20	6	A82791 Sequence 4
C 29	11	55.0	20	6	A83708 Sequence 4
C 30	11	55.0	20	6	BD274392 Human van
C 31	11	55.0	20	6	CQ757498 Sequence
C 32	11	55.0	20	6	AX026882 Sequence
C 33	11	55.0	20	6	BD082732 Intracell
C 34	11	55.0	21	6	CQ831007 Sequence
C 35	11	55.0	21	6	AX077873 Sequence
C 36	11	55.0	22	6	BD102253 Method of
C 37	11	55.0	25	6	AX166683 Sequence
C 38	11	55.0	25	6	AX196821 Sequence
C 39	11	55.0	29	6	BD140471 Secreted
C 40	11	55.0	29	6	BD191485 Secreted
C 41	11	55.0	30	6	AX537725 Sequence
C 42	11	55.0	31	6	CQ868121 Sequence
C 43	11	55.0	36	6	AX512846 Sequence
C 44	11	55.0	42	6	AR021384 Sequence
C 45	11	55.0	42	6	AR042946 Sequence

ALIGNMENTS

RESULT 1
AR356488/c AR356488 54 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 2606 from patent US 6593114.
DEFINITION AR356488
ACCESSION AR356488
VERSION AR356488.1 GI:33762572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 2606 15-JUN-2003;
FEATURES
source Location/Qualifiers
1..54
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 65.0%; Score 13; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 3,4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCAT 16
Db 47 TTGGCACTCCCAT 35

RESULT 2
AR538044/c AR538044 54 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 2606 from patent US 6737248.
DEFINITION AR538044
ACCESSION AR538044
VERSION AR538044.1 GI:53929261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and

TITLE Rosen, C.A.
Staphylococcus aureus polymucleotides and sequences
JOURNAL Patent: US 6737248-A 2606 18-MAY-2004;
FEATURES Location/Qualifiers
source 1..54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCAT 16
Db 47 TTGGCACTCCCAT 35

RESULT 3
LOCUS COS48380 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 18015 from Patent WO0210449.
ACCESSION COS48380
VERSION COS48380.1 GI:41514807
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
FEATURES Patent: WO 0210449-A 18015 07-FEB-2002;
source Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCAT 16
Db 4 TTGGCACTCCCAT 16

RESULT 4
LOCUS AX293633/c 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 5395 from Patent WO0179548.
ACCESSION AX293633
VERSION AX293633.1 GI:17055316
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Barany, F., Zivyl, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
FEATURES Patent: WO 0179548-A 5395 25-OCT-2001;
source CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..20
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
Db 15 GCATTGCCACTC 4

RESULT 5
LOCUS ARI48756 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 113 from patent US 6225451.
ACCESSION ARI48756
VERSION ARI48756.1 GI:15112846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 21)
Ballingier, D.G., Ding, W., Wagner, S. and Hese, M.A.
TITLE Chromosome 11-linked coronary heart disease susceptibility gene
JOURNAL CHD1
FEATURES Patent: US 6225451-A 113 01-MAY-2001;
source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCA 15
Db 2 TTGGCACTCCCA 13

RESULT 6
LOCUS AX289000/c 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 762 from Patent WO0179548.
ACCESSION AX289000
VERSION AX289000.1 GI:17050683
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Barany, F., Zivyl, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
FEATURES Patent: WO 0179548-A 762 25-OCT-2001;
source CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
Db 19 GCATTGCCACTC 8

RESULT 7
AX551638 26 bp DNA linear PAT 26-NOV-2002
LOCUS
DEFINITION Sequence 257 from Patent WO0250276.
ACCESSION AX551638
VERSION AX551638.1 GI:25814437
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 Li, L., Padigaru, M., Ballinger, R.A., Kekuda, R., Colman, S.D.,
Sciore, P., Smithson, G., Peyman, J.A., Macdougall, J.R., Stone, D.,
Vernet, C.A., Shenoy, S., Gunther, E., Millet, I., Tchierney, V.T.,
Anderson, D., Gusev, V., Malyanekar, U.M., Zhong, H., Ellerman, K.E. and
Wolanc, A.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0250276-A 257 27-JUN-2002;
Curagen Corporation (US)
FEATURES
source
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="TaqMan PCR primer"

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
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5 TTGCCACTCCCA 16

RESULT 8
AX703273 26 bp DNA linear PAT 03-APR-2003
LOCUS
DEFINITION Sequence 502 from Patent WO02055313.
ACCESSION AX703273
VERSION AX703273.1 GI:29538319
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 Li, L., Ballinger, R.A., Padigaru, M., Kekuda, R., Colman, S.D.,
Spytek, R.A., Casman, S.J., Vernet, C.A., Shenoy, S.G., Gusev, V.,
Malyanekar, U.M., Edinger, S., Gerlach, V., Smithson, G., Stone, D.J.,
Sciore, P., Macdougall, J.R., Gunther, E., Peyman, J.A., Ellerman, K.,
Gangoli, E.A. and Millet, I.
TITLE G-protein coupled receptors and nucleic acids encoding same
JOURNAL Patent: WO 02059313-A 502 01-AUG-2002;
Curagen Corporation (US)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer Sequence"

ORIGIN
Query Match 60.0%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
|||||
5 TTGCCACTCCCA 16

RESULT 9
AR039144/c 29 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 8 from patent US 5807740.
ACCESSION AR039144
VERSION AR039144.1 GI:5958507
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 29)
TITLE Amaral, M.Catherine. and Chen, J.-L.
JOURNAL Regulators of UCP2 gene expression
Patent: US 5807740-A 8 15-SEP-1998;
Location/Qualifiers
1..29
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 60.0%; Score 12; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
|||||
20 TTGCCACTCCCA 9

RESULT 10
AR065274/c 29 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 8 from patent US 5849514.
ACCESSION AR065274
VERSION AR065274.1 GI:5995490
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 29)
TITLE Amaral, M.Catherine. and Chen, J.-L.
JOURNAL Method of identifying agents that modulate UCP2 promoter activity
Patent: US 5849514-A 8 15-DEC-1998;
Location/Qualifiers
1..29
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 60.0%; Score 12; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
|||||
20 TTGCCACTCCCA 9

RESULT 11
BD061658/c 29 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Regulators of UCP2 gene expression.
ACCESSION BD061658
VERSION BD061658.1 GI:22607263
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 29)
TITLE Amaral, C.M. and Chen, J.L.
JOURNAL Regulators of UCP2 gene expression
Patent: JP 2001507943-A 8 19-JUN-2001;
TULARIK INC

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COMMENT      PN      JP 2001507943-A/8
              PD      19-JUN-2001
              PF      22-APR-1998 JP 1998547120
              PR      25-APR-1997 US 08/846012
              PI      CATHERINE M AMARAL, JIN LONG CHEN
              PC      C12N1/00, C12N5/10, C12N15/11, C12N15/63, C12Q1/02, C12Q1/68 CC
              Strandedness: Double;
              CC      Topology: Linear;
              PH      Key      Location/Qualifiers.
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              /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 TTGCCACTCCCA 15
              |||||
              20 TTGCCACTCCCA 9
Db
RESULT 12
AR128133/c      AR128133      39 bp      DNA      linear      PAT 16-MAY-2001
LOCUS
DEFINITION      Sequence 8 from patent US 6183956.
ACCESSION
AR128133
VERSION
AR128133.1 GI:14115795
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 39)
Sivara, M., Strulovici, B. and Flores, O.A.
High throughput in vitro screening assays for transcription
modulators
JOURNAL
Patent: US 6183956-A 8 06-FEB-2001;
FEATURES
  source      1..39
              /organism="unknown"
              /mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      8 CACTCCCATCTCT 19
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              27 CACTCCCATCTCT 16
Db
RESULT 13
AX116213
LOCUS
DEFINITION      Sequence 1336 from Patent WO0129262.
ACCESSION
AX116213
VERSION
AX116213.1 GI:14033155
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Picolit-Newburg, L. and Pohl, M.
Genotyping reagents, kits and methods of use thereof
JOURNAL
Patent: WO 0129262-A 1336 26-APR-2001;
FEATURES
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              Location/Qualifiers
misc_feature      1..51

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCATTGCCACTC 12
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RESULT 14
AX159371/c      AX159371      51 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION      Sequence 2699 from Patent WO0140521.
ACCESSION
AX159371
VERSION
AX159371.1 GI:14540702
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Shinkens, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 2699 07-JUN-2001;
FEATURES
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misc_feature      1..51
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              /mol_type="unassigned DNA"
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              /note="1 of 2 allelic variants (2700 is other entry)
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 TGCCACTCCCAT 16
              |||||
              45 TGCCACTCCCAT 34
Db
RESULT 15
AX159372/c      AX159372      51 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION      Sequence 2700 from Patent WO0140521.
ACCESSION
AX159372
VERSION
AX159372.1 GI:14540703
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Shinkens, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 2700 07-JUN-2001;
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              /mol_type="unassigned DNA"
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ORIGIN

/note="2 of 2 allelic variants (2699 is other entry)
Accession number cg42330545"

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCAT 16
|||||
Db 45 TGGCACTCCCAT 34

RESULT 16

AX159373/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 2701 from Patent WO0140521.
DEFINITION AX159373
ACCESSION AX159373.1 GI:14540704
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2701 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="1 of 2 allelic variants (2702 is other entry)
Accession number cg42330545"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCAT 16
|||||
Db 35 TGGCACTCCCAT 24

RESULT 17
AX165283/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 478 from Patent WO0138586.
DEFINITION AX165283
ACCESSION AX165283.1 GI:14546112
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 478 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="single nucleotide polymorphism

ORIGIN

Accession number cg44005525"

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
|||||
Db 27 GCATTGCCACTC 16

RESULT 18

HUMUT5280A 55 bp DNA linear STS 28-DEC-1994
LOCUS Human STS UT5280, 5' primer bind, sequence tagged site.
DEFINITION L30822
ACCESSION L30822.1 GI:604659
VERSION
KEYWORDS STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; mononucleotide repeat; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Gerken, S.C., Matsunami, N., Plackett, R., Albertsen, H., Ballard, L., Wells, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsnert, T., Tingey, A., Lalouel, J.-M. and White, R.
TITLE Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
JOURNAL Unpublished (1994)
COMMENT Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: steecorona.med.utah.edu
Primer A: CACTCAGCCTGGCAATVAGAG
Primer B: GTAGCTCTGTTGCACATGACACT
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 94 94
C 10 sec. 60 C 10 sec. 72 C 20 sec. 30
70 C 10 sec. 72 C 20 sec. Mg++: 1.50 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 3.

FEATURES

source 1. .55
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="8"
11.33
primer_bind
/evidence=experimental

ORIGIN

Query Match 60.0%; Score 12; DB 11; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCACTCC 13
|||||
Db 5 CATTGCCACTCC 16

RESULT 19

COS45434/c 60 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 15069 from Patent WO0210449.
DEFINITION COS45434
ACCESSION COS45434.1 GI:41511698
VERSION
KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE	Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL	Patent: WO 0210449-A 15069 07-FEB-2002;
COMPUGEN INC. (US)	
FEATURES	
SOURCE	Location/Qualifiers
	1..60
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
ORIGIN	
Query Match	60.0%; Score 12; DB 6; Length 60;
Best Local Similarity	100.0%; Pred. No. 1.4e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	9 ACTGCCATCTT 20
Db	17 ACTGCCATCTT 6
RESULT 20	
CQ547633	60 bp DNA linear PAT 30-JAN-2004
LOCUS	CQ547633
DEFINITION	Sequence 17268 from Patent WO0210449.
ACCESSION	CQ547633
VERSION	CQ547633.1 GI:41513897
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1
AUTHORS	Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE	Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL	Patent: WO 0210449-A 17268 07-FEB-2002;
COMPUGEN INC. (US)	
FEATURES	
SOURCE	Location/Qualifiers
	1..60
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
ORIGIN	
Query Match	60.0%; Score 12; DB 6; Length 60;
Best Local Similarity	100.0%; Pred. No. 1.4e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCATTGCCATCT 12
Db	44 GCATTGCCATCT 55
RESULT 21	
LOCUS	AY139609 66 bp DNA linear PRI 21-OCT-2002
DEFINITION	Homo sapiens dytrophin (DMD) gene deletion breakpoint junction 04.
ACCESSION	AY139609
VERSION	AY139609.1 GI:24209751
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 66)
AUTHORS	Strom,M., Pozzoli,U., Cagliani,R., Giorda,R., Comi,G.P., Bardoni,A., Menozzi,G. and Bresolin,N.

TITLE		Relevance of sequence and structure elements for deletion events in the dystrophin gene major hot-spot	
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 66)		
AUTHORS	Sironi,M., Pozzoli,U., Cagliani,R., Giorda,R., Comi,G.P., Bardoni,A., Menozzi,G. and Bresolin,N.		
TITLE	Direct Submision		
JOURNAL	Submitted (06-AUG-2002) I.R.C.C.S. E.Medea, Ass. La Nostra Famiglia, Via Don L. Monza, 20, Bosisio Parini, LC 23842, Italy		
FEATURES	Location/Qualifiers		
source	1..66		
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>66 /gene="DMD" /note="dystrophin"		
intron	<1..30 /gene="DMD" /number=44		
misc_recomb	31..35 /gene="DMD" /note="deletion breakpointjunction 04"		
intron	36..>66 /gene="DMD" /number=48		
ORIGIN			
Query Match	60.0%; Score 12; DB 9; Length 66;		
Best Local Similarity	100.0%; Pred. No. 1.3e+04;		
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	9 ACTCCCATCTT 20		
Db	48 ACTCCCATCTT 59		
RESULT 22			
LOCUS	AR040149 17 bp DNA linear PAT 29-SEP-1999		
DEFINITION	Sequence 997 from patent US 5807743.		
ACCESSION	AR040149		
VERSION	AR040149.1 GI:5959512		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 17)		
TITLE	Stinchcomb,D.T. and McSwiggen,J.A.		
JOURNAL	Interleukin-2 receptor gamma-chain ribozymes		
FEATURES	Patent: US 5807743-A 997 15-SEP-1998; Location/Qualifiers 1..17 /organism="unknown" /mol_type="unassigned DNA"		
ORIGIN			
Query Match	55.0%; Score 11; DB 6; Length 17;		
Best Local Similarity	100.0%; Pred. No. 6e+04;		
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	2 CATTGCCACTC 12		
Db	6 CATTGCCACTC 16		
RESULT 23			
LOCUS	AR241626 18 bp DNA linear PAT 20-DEC-2002		
DEFINITION	Sequence 5 from patent US 6471964.		
ACCESSION	AR241626		
VERSION	AR241626.1 GI:27287383		
KEYWORDS	.		

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Biering, E. and Krososoy, B.
TITLE DNA encoding structural protein-1 of infectious Salmon Anaemia virus and uses thereof
JOURNAL Patent: US 6471964-A 5 29-OCT-2002;
FEATURES
source
1. 18
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
|||||
15 TGGCACTCCCA 5

Db 15 TGGCACTCCCA 5

RESULT 24
AR258715/c 18 bp DNA linear PAT 20-DEC-2002
LOCUS AR258715
DEFINITION Sequence 5 from patent US 6489163.
ACCESSION AR258715
VERSION AR258715.1 GI:27309121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Roy, A.K. and Chen, S.
TITLE Ribozyme mediated inactivation of the androgen receptor
JOURNAL Patent: US 6489163-A 5 03-DEC-2002;
FEATURES
source
1. 18
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
|||||
13 TGGCACTCCCA 3

Db 13 TGGCACTCCCA 3

RESULT 25
AX137953/c 18 bp DNA linear PAT 30-MAY-2001
LOCUS AX137953
DEFINITION Sequence 5 from Patent EPI094069.
ACCESSION AX137953
VERSION AX137953.1 GI:14274051
KEYWORDS
SOURCE Infectious salmon anemia virus
ORGANISM Infectious salmon anemia virus
REFERENCE 1
AUTHORS Biering, E. and Krososoy, B.
TITLE Dna encoding structural protein-1 of infectious salmon anaemia virus and uses thereof
JOURNAL Patent: EP 1094069-A 5 25-APR-2001;
FEATURES
source
1. 18
/organism="Infectious salmon anemia virus"
/mol_type="unassigned DNA"

ORIGIN primer_bind /db_xref="taxon:55987"
1. 18

Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
|||||
15 TGGCACTCCCA 5

Db 15 TGGCACTCCCA 5

RESULT 26
BD015843/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD015843
DEFINITION DNA encoding structure protein-1 of infectious salmon anemia virus and utilization thereof.
ACCESSION BD015843
VERSION BD015843.1 GI:22556980
KEYWORDS JP 2001211888-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Eric, B.A. and Beyorn, K.B.
TITLE DNA encoding structure protein-1 of infectious salmon anemia virus and utilization thereof
JOURNAL Patent: JP 2001211888-A 2 07-AUG-2001;
COMMENT AKZO NOBEL NV
OS Infectious salmon anaemia virus
PN JP 2001211888-A/2
PD 07-AUG-2001
PF 17-OCT-2000 JP 2000316583
PR 18-OCT-1999 EP 99203401.7
PI BILLING A ERIC KLOSSEI B BEYORN
PC C12N15/09, A61K38/00, A61K39/145, A61P31/12, C07K14/11, C07K16/10, C12Q1/68,
PC G01N33/569//C12P21/08, C12N15/00, A61K37/02
CC DNA encoding structure protein-1 of infectious salmon anemia virus and
CC utilization thereof
CC primer_bind (1). (18).
FH Key Location/Qualifiers
FT primer_bind (1). (18).
FEATURES
source
1. 18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
|||||
15 TGGCACTCCCA 5

Db 15 TGGCACTCCCA 5

RESULT 27
AR174747 19 bp DNA linear PAT 17-DEC-2001
LOCUS AR174747
DEFINITION Sequence 46 from patent US 6307035.
ACCESSION AR174747
VERSION AR174747.1 GI:17915067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Rauscher, F.J. III and Jensen, D.E.
TITLE BRCA1 associated polynucleotide (BAP-1) and uses thereof

JOURNAL Patent: US 6307035-A 46 23-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 ORIGIN /mol_type="unassigned DNA"

Query Match 55.0%; Score 11; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCAT 17
 |||||
 Db 6 CCACTCCCAT 16

RESULT 28
 A82791/c 20 bp DNA linear PAT 21-JAN-2000

LOCUS A82791
 DEFINITION Sequence 4 from Patent EP0884385.
 ACCESSION A82791
 VERSION A82791.1 GI:6732470

KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Riccardo C.

TITLE Intracellular modulators of apoptotic cell death pathways
 JOURNAL Patent: EP 0884385-A 4 16-DEC-1998;
 APPLIED RESEARCH SYSTEMS (AN)

FEATURES Location/Qualifiers
 source 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGCCACTCCCA 15
 |||||
 Db 18 TGCCACTCCCA 8

RESULT 29
 A83708/c 20 bp DNA linear PAT 21-JAN-2000

LOCUS A83708
 DEFINITION Sequence 4 from Patent WO9849291.
 ACCESSION A83708
 VERSION A83708.1 GI:6732944

KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Riccardo C.

TITLE INTRACELLULAR GLUCOCORTICOID-INDUCED LEUCINE ZIPPER MODULATORS OF
 JOURNAL APOPTIC CELL DEATH PATHWAYS
 Patent: WO 9849291-A 4 05-NOV-1998;
 RICCARDI CARLO (IT); APPLIED RESEARCH SYSTEMS (NL)

FEATURES Location/Qualifiers
 source 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGCCACTCCCA 15
 |||||
 Db 18 TGCCACTCCCA 8

RESULT 30
 BD274392 20 bp DNA linear PAT 17-JUL-2003

LOCUS BD274392
 DEFINITION Human vanilloid receptor and use thereof.
 ACCESSION BD274392
 VERSION BD274392.1 GI:33084160

KEYWORDS JP 2002531085-A/29.
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 20)
 AUTHORS Delany, N.S., Sansau, P. and Tate, S.N.

TITLE Human vanilloid receptor and use thereof
 JOURNAL Patent: JP 2002531085-A 29 24-SEP-2002;
 GLAXO GROUP LTD

COMMENT OS Artificial Sequence
 PN JP 2002531085-A/29
 PD 24-SEP-2002

PF 30-NOV-1999 JP 2000585397
 PR 01-DEC-1998 GB 9826359.3

PI NATALIE SAMANTHA DELANY, PHILIPPE SANSEAU, SIMON NICHOLAS TATE
 PC C12N15/09,A61K45/00,A61P1/00,A61P11/06,A61P13/00, PC
 A61P19/00,
 PC A61P25/04,A61P25/06,A61P25/28,A61P29/00,A61P29/00,C07K14/705,
 PC C07K16/28,
 PC C12N5/10,C12P21/02,C12Q1/02/(C12P21/02,C12R1:91),C12N15/00,
 PC C12N5/00

CC Description of Artificial Sequence: Primer
 FH Key
 FT source 1..20
 Location/Qualifiers

FEATURES Location/Qualifiers
 source 1..20
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCCTTCCTT 20
 |||||
 Db 5 CTCCTTCCTT 15

RESULT 31
 CQ757498/c 20 bp DNA linear PAT 01-MAR-2004

LOCUS CQ757498
 DEFINITION Sequence 9 from Patent WO2003107249.
 ACCESSION CQ757498
 VERSION CQ757498.1 GI:44847536

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1
 AUTHORS Kotani, H. and Mizunari, S.

TITLE Method for predicting a drug transport capability by abcg2
 JOURNAL polymorphisms
 Patent: WO 2003107249-A 9 24-DEC-2003;
 BANYU PHARMACEUTICAL CO., LTD. (JP)

FEATURES Location/Qualifiers
 source 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN /db_xref="taxon:32630"
/note="Exon 4 forward primer"

Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTCGCATTCTT 20
18 CTCGCATTCTT 8
Db 18 CTCGCATTCTT 8

RESULT 32
AX026882 20 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 35 from Patent WO0032766.
DEFINITION AX026882
ACCESSION AX026882 GI:10187981
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Delany,N.S.; Tate,S.N. and Saneau,P.
TITLE Human vanilloid receptors and their uses
JOURNAL Patent: WO 0032766-A 35 08-JUN-2000;
DELANY NATALIE SAMANTHA (GB) ; TATE SIMON NICHOLAS (GB) ; GLAXO
GROUP LTD (GB) ; SANEAU PHILIPPE (GB)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTCGCATTCTT 20
5 CTCGCATTCTT 15
Db 5 CTCGCATTCTT 15

RESULT 33
BD082732/c 20 bp DNA linear PAT 27-AUG-2002
LOCUS BD082732
DEFINITION Intracellular modulator in apoptosis cell death pathway.
ACCESSION BD082732
VERSION BD082732.1 GI:22628342
KEYWORDS JP 2001523102-A/3.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Riccardi,C.
TITLE Intracellular modulator in apoptosis cell death pathway
JOURNAL Patent: JP 2001523102-A 3 20-NOV-2001;
APPLIED RESEARCH SYSTEMS ARS HOLDING NV
COMMENT OS Mus sp. (mouse)
PN JP 2001523102-A/3
PD 20-NOV-2001
PF 27-APR-1998 JP 1998546599
PR 28-APR-1997 EP 97107033.9
PI CARLO RICCARDI
PC C12N15/12,C07K14/47,G01N33/50,A61K38/17,A61K48/00,C12N5/10 CC
PER reverse primer Location/Qualifiers
FH Key Location/Qualifiers
1..20

FEATURES
source 1..20

ORIGIN /organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
18 TGGCACTCCCA 8
Db 18 TGGCACTCCCA 8

RESULT 34
CO831007 21 bp DNA linear PAT 29-JUL-2004
LOCUS CO831007
DEFINITION Sequence 92 from Patent EP1437417.
ACCESSION CO831007
VERSION CO831007.1 GI:50831142
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Park,J.G., Kim,I.J., Kang,H.C. and Park,J.H.
TITLE Beta-catenin oligonucleotide microchip and method for detecting
JOURNAL beta-catenin mutations employing same
Patent: EP 1437417-A 92 14-JUL-2004;
National Cancer Center (KR)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
4 TGGCACTCCCA 14
Db 4 TGGCACTCCCA 14

RESULT 35
AX077873/c 21 bp DNA linear PAT 22-FEB-2001
LOCUS AX077873
DEFINITION Sequence 29 from Patent WO0105957.
ACCESSION AX077873
VERSION AX077873.1 GI:13157720
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Good,X.C. and Monte,J.
TITLE Grapevine leafroll-associated virus proteins
JOURNAL Patent: WO 0105957-A 29 25-JAN-2001;
AGRITOPPE, INC. (US)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
4 TGGCACTCCCA 14
Db 4 TGGCACTCCCA 14

```
OY      9  ACTCCCATCTCT 19
      |||||
Db      18  ACTCCCATCTCT 8

RESULT 36
LOCUS    BD102253
DEFINITION Method of detecting risk factor for onset of arteriosclerosis.
ACCESSION BD102253
VERSION   BD102253.1 GI:22647827
KEYWORDS  WO 0171032-A/16.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS   Nagano,M., Ito,M., Sagenashi,Y., Hattori,H., Egashira,T.,
           Yamashita,S. and Matsumura,Y.
           Method of detecting risk factor for onset of arteriosclerosis
           Patent: WO 0171032-A 16 27-SEP-2001,
           BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGENASHI, HIROAKI HATTORI,
           TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
COMMENT   OS Homo sapiens (human)
           PN WO 0171032-A/16
           PD 27-SEP-2001
           PF 23-MAR-2001 WO 2001JP002327
           PI 24-MAR-2000 JP 00P 084264
           PI MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGENASHI, HIROAKI HATTORI, TORU

FEATURES
  source          1..22
                   /organism="Homo sapiens (human)".
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"

ORIGIN
Query Match      55.0%; Score 11; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      5  TGGCAGTCCCA 15
      |||||
Db      1  TGGCAGTCCCA 11

RESULT 37
LOCUS    AX166683/c
DEFINITION Sequence 174 from Patent WO0138503.
ACCESSION AX166683
VERSION   AX166683.1 GI:14546958
KEYWORDS
SOURCE    synthetic construct
           other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarshanam,S.S., Martinez,R.,
           Flanagan,P. and Clary,D.S.
           Novel human protein kinases and protein kinase-like enzymes
           Patent: WO 0138503-A 174 31-MAY-2001,
           Sugen, Inc. (US)
COMMENT   Location/Qualifiers
           1..25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"

OY      9  ACTCCCATCTCT 19
      |||||
Db      18  ACTCCCATCTCT 8

RESULT 38
LOCUS    AX196821
DEFINITION Sequence 528 from Patent WO0151627.
ACCESSION AX196821
VERSION   AX196821.1 GI:15387027
KEYWORDS  Glycine max (soybean)
SOURCE    Glycine max (soybean)
ORGANISM  Glycine max
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
           Glycine.
REFERENCE 1
AUTHORS   Haugbe,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
           Nucleic acid molecules and other molecules associated with soybean
           cyst nematode resistance
           Patent: WO 0151627-A 528 19-JUL-2001;
           MONSANTO COMPANY (US)
COMMENT   Location/Qualifiers
           1..25
           /organism="Glycine max"
           /mol_type="unassigned DNA"
           /db_xref="taxon:3847"
           /note="Seq ID: 240017_region_G3_35078_13_Reverse_Primer"

ORIGIN
Query Match      55.0%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      10  CTCCCATCTCT 20
      |||||
Db      1  CTCCCATCTCT 11

RESULT 39
LOCUS    BD140471
DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD140471
VERSION   BD140471.1 GI:23235416
KEYWORDS  JP 2002506611-A/21.
SOURCE    synthetic construct
           other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS   Jacobs,K., McCoy,J.M., Lavalite,E.R., Racie,L.A.C., Evans,C.,
           Merberg,D., Treacy,M., Agostino,M.J., Il,R.J.S., Wong,G.G.,
           Clark,H.F. and Fechtel,K.
           Secreted proteins and polynucleotides encoding them
           Patent: JP 2002506611-A 21 05-MAR-2002;
           GENETICS INSTITUTE INC
COMMENT   OS Artificial Sequence
           PN JP 2002506611-A/21
           PD 05-MAR-2002
           PF 24-NOV-1998 JP 2000522118
           PI 26-NOV-1997 US 60/066804 23-NOV-1998 US 09/197886 PI
           KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALITE, LISA A COLLINS
           RACIE,
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PI CHERYL EVANS, DAVID MERBERG, MAURICE TREACY, MICHAEL J AGOSTINO,
PI ROBERT J STEININGER II, GORDON G WONG, HILARY F CLARK, KIM PI
FECHTEL
PC C12N15/09, C07K14/00, C12N1/21, C12N5/10, C12P19/34, C12P21/02, PC
C12Q1/68//
PC A61P29/00, A61P35/00, A61P37/04, A61P37/06, C12N15/00, C12N5/00 CC
oligonucleotide
CC biotinylated phosphoramidite residue
FH Key Location/Qualifiers
FT misc feature (2).
Location/Qualifiers
1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
|||||
DB 8 TGGCACTCCCA 18

RESULT 40
BD191485 29 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Accession
BD191485
BD191485.1 GI:33001224
VERSION
JP 2002510196-A/12.
KEYWORDS
unidentified
SOURCE
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 29)
Jacobson, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.
Secreted proteins and polynucleotides encoding them
Patent: JP 2002510196-A 12 02-APR-2002;
GENETICS INSTITUTE INC
PN JP 2002510196-A/12
PD 02-APR-2002
PF 14-APR-1998 JP 1998544380
PR 15-APR-1997 US 08/843374.13-APR-1998 US 09/059487 PI
KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C07K14/47, A61K38/17
CC Strandedness: Single;
CC Topology: linear;
CC /desc=Oligonucleotide;
FH Key Location/Qualifiers
1. .29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACT 11
|||||
DB 14 GCATTGCCACT 24

ORIGIN

RESULT 41
AX537725/c 30 bp DNA linear PAT 23-NOV-2002
LOCUS
AX537725

Query Match 55.0%; Score 11; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACT 11
|||||
DB 14 GCATTGCCACT 24

RESULT 41
AX537725/c 30 bp DNA linear PAT 23-NOV-2002
LOCUS
AX537725

DEFINITION Sequence 4 from Patent WO02072845.
ACCESSION AX537725
AX537725.1 GI:25269719
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
Chafield, S.N.
Salmonella promoter for heterologous gene expression
Patent: WO 02072845-A 4 19-SEP-2002;
Microscience Limited (GB)
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCACTC 12
|||||
DB 23 CATTGCCACTC 13

RESULT 42
CQ868121 31 bp DNA linear PAT 13-SEP-2004
LOCUS
DEFINITION
Accession
CQ868121
CQ868121 Sequence 338 from Patent WO2004074318.
VERSION
CQ868121.1 GI:51998173
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
Dautry-Varstat, A. and Subtil-Sands, A.
Secreted chlamydia polypeptides, polynucleotides coding
therefor, therapeutic and diagnostic uses thereof
Patent: WO 2004074318-A 338 02-SEP-2004;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
(CNRS) (FR)
Location/Qualifiers
1. .31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGCATTCTT 20
|||||
DB 18 CTCGCATTCTT 28

RESULT 43
AX512846 36 bp DNA linear PAT 03-OCT-2002
LOCUS
DEFINITION
Accession
AX512846
AX512846 Sequence 1 from Patent WO02062943.
VERSION
AX512846.1 GI:23504029
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

Query Match 55.0%; Score 11; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGCATTCTT 20
|||||
DB 18 CTCGCATTCTT 28

RESULT 43
AX512846 36 bp DNA linear PAT 03-OCT-2002
LOCUS
DEFINITION
Accession
AX512846
AX512846 Sequence 1 from Patent WO02062943.
VERSION
AX512846.1 GI:23504029
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Malvy, C., Makeienko, A.C. and Gottikh, M.
 TITLE Use of oligonucleotides for improving plasmid transfection in
 cells, transfection method and kit
 JOURNAL Patent: WO 02062943-A 1 15-AUG-2002;
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR); INSTITUT
 GUSTAVE ROUSSY (FR)

FEATURES
 source Location/Qualifiers
 1..36
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCCACTCC 13
 |||||
 Db 24 ATTGCCACTCC 34

RESULT 44
 AR021384/c AR021384 42 bp DNA linear PAT 05-DEC-1998
 LOCUS Sequence 32 from patent US 5789650.
 DEFINITION AR021384
 ACCESSION AR021384
 VERSION AR021384.1 GI:3975999
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 42)
 TITLE Lomborg, N. and Kay, R.M.
 JOURNAL Transgenic non-human animals for producing heterologous antibodies
 FEATURES Patent: US 5789650-A 32 04-AUG-1998;
 source Location/Qualifiers
 1..42
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
 |||||
 Db 11 CACTCCCATTC 1

RESULT 45
 AR042946/c AR042946 42 bp DNA linear PAT 29-SEP-1999
 LOCUS Sequence 32 from patent US 5814318.
 DEFINITION AR042946
 ACCESSION AR042946
 VERSION AR042946.1 GI:5963954
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 42)
 TITLE Lomborg, N. and Kay, R.M.
 JOURNAL Transgenic non-human animals for producing heterologous antibodies
 FEATURES Patent: US 5814318-A 32 29-SEP-1998;
 source Location/Qualifiers
 1..42
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CACTCCCATTC 18
 |||||
 Db 11 CACTCCCATTC 1

Search completed: September 14, 2005, 11:03:30
 Job time : 2625 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 06:00:04 ; Search time 373 Seconds
(without alignments)
317.412 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20

Sequence: 1 gcattgccaccatccatctt 20

Scoring table: OLIGO_NUC

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4427878

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001a:*
5: geneseq2002a:*
6: geneseq2002b:*
7: geneseq2003a:*
8: geneseq2003b:*
9: geneseq2003c:*
10: geneseq2003d:*
11: geneseq2003e:*
12: geneseq2004a:*
13: geneseq2004b:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	65.0	54	AAV76917	AAV76917 Staphyloc
C 2	13	65.0	60	ABN45267	ABN45267 Human spl
C 3	12	60.0	12	ABH69241	ABH69241 Oligonuc
C 4	12	60.0	12	ABH67956	ABH67956 Oligonuc
C 5	12	60.0	20	AB193675	AB193675 Capture o
C 6	12	60.0	20	ADN31408	ADN31408 Human for
C 7	12	60.0	20	ADN31409	ADN31409 Human for
C 8	12	60.0	20	ADN31527	ADN31527 Human for
C 9	12	60.0	21	AAZ26938	AAZ26938 Human chr
C 10	12	60.0	22	AD31699	AD31699 Gene expr
C 11	12	60.0	24	AB183921	AB183921 Capture o
C 12	12	60.0	24	AB183920	AB183920 Capture o
C 13	12	60.0	26	AB559154	AB559154 Human G-P
C 14	12	60.0	26	ABQ88545	ABQ88545 Human GPC
C 15	12	60.0	26	AD104496	AD104496 Human G-P
C 16	12	60.0	29	AAV44981	AAV44981 PCR prime
C 17	12	60.0	39	AAV08886	AAV08886 PCR prime
C 18	12	60.0	39	AAZ28769	AAZ28769 G-less ol
C 19	12	60.0	41	AA155696	AA155696 Human zin
C 20	12	60.0	51	AA175760	AA175760 Human sil

C 21	12	60.0	51	4	AA175759	AA175759 Human sil
C 22	12	60.0	51	4	AA175758	AA175758 Human sil
C 23	12	60.0	51	4	AA138540	AA138540 Human SNP
C 24	12	60.0	51	5	AB100487	AB100487 Human sil
C 25	12	60.0	60	6	ABN44520	ABN44520 Human spl
C 26	12	60.0	60	6	ABN42321	ABN42321 Human spl
C 27	11	55.0	13	5	ABF27951	ABF27951 Oligonuc
C 28	11	55.0	13	5	ABF27950	ABF27950 Oligonuc
C 29	11	55.0	13	5	ABF27950	ABF27950 Oligonuc
C 30	11	55.0	13	5	ABF27950	ABF27950 Oligonuc
C 31	11	55.0	13	5	ABF27950	ABF27950 Oligonuc
C 32	11	55.0	18	8	ABA95013	ABA95013 ISAV stru
C 33	11	55.0	18	8	ABA95013	ABA95013 ISAV stru
C 34	11	55.0	18	8	ABA95013	ABA95013 ISAV stru
C 35	11	55.0	18	8	ABA95013	ABA95013 ISAV stru
C 36	11	55.0	20	2	AAV80303	AAV80303 Vector pc
C 37	11	55.0	20	3	AAV80303	AAV80303 Vector pc
C 38	11	55.0	20	3	AAV80303	AAV80303 Vector pc
C 39	11	55.0	20	9	ADA24256	ADA24256 Major all
C 40	11	55.0	20	12	AD157250	AD157250 ATP-bind
C 41	11	55.0	20	12	ADK96200	ADK96200 Primer of
C 42	11	55.0	20	12	ADN31407	ADN31407 Human for
C 43	11	55.0	20	12	ADN89393	ADN89393 Human CD2
C 44	11	55.0	21	2	AAQ76368	AAQ76368 Oligonuc
C 45	11	55.0	21	4	AAA91279	AAA91279 GRav-5 n

ALIGNMENTS

RESULT 1
AAV76917/c
ID AAV76917 standard; DNA; 54 BP.
XX
AC AAV76917;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus contig SEQ ID #2606.
XX
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX
OS Staphylococcus aureus.
XX
PN EP786519-A2.
XX
PD 30-JUL-1997.
XX
PF 07-JAN-1997; 97BP-00100117.
XX
PR 05-JAN-1996; 96US-0009661P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
DR WPI; 1997-374922/35.
XX
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX
PT stored on computer readable medium and used in the production of anti-
XX
PT S. aureus vaccines.
XX
PS Claim 1; Page 2287; 3271pp; English.
XX
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S. aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or

CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against *S. aureus* infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the *S. aureus* DNA sequences contained on the computer
CC readable medium
SQ Sequence 54 BP; 18 A; 4 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGGCACTCCCAT 16
Db 47 TTGGCACTCCCAT 35

RESULT 2
ABN45267
ID ABN45267 standard; DNA; 60 BP.

AC ABN45267;
XX
DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:18015.

KM Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0231607P.

PR 02-MAY-2001; 2001US-0287724P.

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.

PS Example 1; SEQ ID NO 18015; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 60 BP; 12 A; 14 C; 15 G; 19 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGGCACTCCCAT 16
Db 4 TTGGCACTCCCAT 16

RESULT 3
ABH69241/c
ID ABH69241 standard; DNA; 12 BP.

AC ABH69241;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 269218 for detecting SNP TSC0001665.

KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

OS central nervous system; gastrointestinal; respiratory; immune; metabolic.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piegenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 269218; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTGCCATTCT 19
DB 12 CACTGCCATTCT 1

RESULT 4
ABH67956.
ID ABH67956 standard; DNA; 12 BP.
XX
XX
AC ABH67956;
XX

DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 267933 for detecting SNP TSC0000710.
XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

XX Homo sapiens.
XX
XX MO200177384-A2.
XX

PD 18-OCT-2001.
XX

XX 06-APR-2001; 2001MO-1B000713.
XX

XX 07-APR-2000; 2000DB-01019173.
XX

XX (EPIC-) EPIGENOMICS AG.
XX

XX Olek A, Piepenbrock C, Berlin K;
XX

XX WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

XX Claim 1; SEQ ID NO 267933; 29pp + Sequence Listing; German.
XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
SQ

Query Match 60.0%; Score 12; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTGCCATTCT 18
DB 1 CCACTGCCATTCT 12

RESULT 5
ABI93675/c
ID ABI93675 standard; DNA; 20 BP.

XX
XX ABI93675;
AC

XX 16-FEB-2002 (first entry)
XX
XX
XX

DE Capture oligonucleotide Zip ID#762 oligo #9.
XX

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1, BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX

XX Synthetic.
XX

XX MO200179548-A2.
XX

XX 25-OCT-2001.
XX

XX 04-APR-2001; 2001MO-US010958.
XX

XX 14-APR-2000; 2000US-0197271P.
XX

XX (CORR) CORNELL RES FOUND INC.
XX

XX Barany F, Zirvi M, Gerry NP, Favis R, Kilman R;
XX

XX WPI; 2002-034366/04.
XX

PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX

XX Example 5; Fig 29; 300pp; English.
XX

XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridize with little mismatch, where
XX CC (I) have melting temperatures within a narrow range. The method is useful
XX CC for detecting infectious diseases caused by bacterial infectious agents
XX CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
XX CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX CC Epstein-Barr virus and polio virus, and parasitic infectious agents
XX CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX CC medinensis. The method is also useful for detecting genetic diseases such
XX CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX CC involved in DNA amplification, replication, recombination or repair, the
XX CC cancer is specifically associated with a gene selected from BRCA1 gene,
XX CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX CC method is also used for environmental monitoring, forensics and the food
XX CC and feed industry, detecting comprises scanning (using e.g. a scanning
XX CC electron microscope and infrared microscope) the support at the
XX CC particular sites and identifying (using a computer) identified ligations to a
XX CC beads occurred or absence of the target nucleotide sequences. ABI82074 to
XX CC AB197546 represent oligonucleotide sequences used in the exemplification
XX CC of the present invention
XX

XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
SQ

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTTC 12
DB 15 GCATTGCCACTTC 4

RESULT 6
ADN31408
ID ADN31408 standard; DNA; 20 BP.

```
XX AC ADN31408;
XX DT 12-AUG-2004 (first entry)
XX DE Human forkhead box C2 antisense oligonucleotide ISIS227188.
XX
XX Human; ss; antisense; forkhead box C2; developmental disorder;
XX lymphedema; lymphedema-distichiasis; dysgenesis; iridocorneal angle;
XX Axenfeld-Rieger anomaly; congenital glaucoma.
XX
XX Homo sapiens.
XX OS
XX FH Key
XX FT modified_base
XX FT 1..20
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methylcytidines"
XX FT modified_base
XX FT 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX FT modified_base
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX
XX PN US2004102621-A1.
XX PD 27-MAY-2004.
XX PF 21-NOV-2002; 2002US-00303635.
XX PR 21-NOV-2002; 2002US-00303635.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Double KW;
XX
XX WPI; 2004-399740/37.
XX
XX New compound targeted to a nucleic acid molecule encoding forkhead box
XX C2, useful in diagnosing and treating developmental disorder.
XX
XX Example 15; SEQ ID NO 73; 80bp; English.
XX
XX The invention relates to a new compound 8-80 nucleobases in length (an
XX antisense oligonucleotide) targeted to a nucleic acid molecule encoding
XX forkhead box C2, where the compound specifically hybridizes with the
XX nucleic acid molecule encoding human forkhead box C2 appearing as
XX ADN31339 and inhibits the expression of forkhead box C2. Also included
XX are inhibiting the expression of forkhead box C2 in cells or tissues,
XX screening for a modulator of forkhead box C2, a diagnostic method for
XX identifying a disease state, a kit or assay device comprising the
XX compound and treating an animal having a disease or condition associated
XX with forkhead box C2. The compound and methods are useful in diagnosing
XX and treating developmental disorders e.g. lymphedemas such as lymphedema-
XX distichiasis, dysgenesis of the mouse iridocorneal angle similar to those
XX seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
XX present sequence is an antisense oligonucleotide targeting forkhead box
XX C2.
XX
XX SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 12; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 7
ADN31409
ID ADN31409 standard; DNA; 20 BP.
XX
XX AC ADN31409;
XX
XX DT 12-AUG-2004 (first entry)
XX DE Human forkhead box C2 antisense oligonucleotide ISIS227189.
XX
XX Human; ss; antisense; forkhead box C2; developmental disorder;
XX lymphedema; lymphedema-distichiasis; dysgenesis; iridocorneal angle;
XX Axenfeld-Rieger anomaly; congenital glaucoma.
XX
XX Homo sapiens.
XX OS
XX FH Key
XX FT modified_base
XX FT 1..20
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methylcytidines"
XX FT modified_base
XX FT 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX FT modified_base
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX
XX PN US2004102621-A1.
XX PD 27-MAY-2004.
XX PF 21-NOV-2002; 2002US-00303635.
XX PR 21-NOV-2002; 2002US-00303635.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Double KW;
XX
XX WPI; 2004-399740/37.
XX
XX New compound targeted to a nucleic acid molecule encoding forkhead box
XX C2, useful in diagnosing and treating developmental disorder.
XX
XX Example 15; SEQ ID NO 74; 80bp; English.
XX
XX The invention relates to a new compound 8-80 nucleobases in length (an
XX antisense oligonucleotide) targeted to a nucleic acid molecule encoding
XX forkhead box C2, where the compound specifically hybridizes with the
XX nucleic acid molecule encoding human forkhead box C2 appearing as
XX ADN31339 and inhibits the expression of forkhead box C2. Also included
XX are inhibiting the expression of forkhead box C2 in cells or tissues,
XX screening for a modulator of forkhead box C2, a diagnostic method for
XX identifying a disease state, a kit or assay device comprising the
XX compound and treating an animal having a disease or condition associated
XX with forkhead box C2. The compound and methods are useful in diagnosing
XX and treating developmental disorders e.g. lymphedemas such as lymphedema-
XX distichiasis, dysgenesis of the mouse iridocorneal angle similar to those
XX seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
XX present sequence is an antisense oligonucleotide targeting forkhead box
XX C2.
XX
XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 12; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GCATTGCCACTC 12
 DB 9 GCATTGCCACTC 20

RESULT 8
 ID ADN31527/c
 ID ADN31527 standard; cDNA; 20 BP.

ADN31527;

12-AUG-2004 (first entry)

Human forkhead box C2 cDNA AS target region #25.

Human; ss; antisense; forkhead box C2; developmental disorder;
 lymphoedema; lymphoedema-distichiasis; dysgenesis; iridocorneal angle;
 Axenfeld-Rieger anomaly; congenital glaucoma.

Homo sapiens.

US2004102621-A1.

27-MAY-2004.

21-NOV-2002; 2002US-00303635.

21-NOV-2002; 2002US-00303635.

(ISIS-) ISIS PHARM INC.

Doble KW;

WPI; 2004-399740/37.

New compound targeted to a nucleic acid molecule encoding forkhead box
 C2, useful in diagnosing and treating developmental disorder.

Example 16; SEQ ID NO 192; 80bp; English.

The invention relates to a new compound 8-80 nucleobases in length (an
 antisense oligonucleotide) targeted to a nucleic acid molecule encoding
 forkhead box C2, where the compound specifically hybridises with the
 nucleic acid molecule encoding human forkhead box C2 appearing as
 AN31339 and inhibits the expression of forkhead box C2. Also included
 are inhibiting the expression of forkhead box C2 in cells or tissues,
 screening for a modulator of forkhead box C2, a diagnostic method for
 identifying a disease state, a kit or assay device comprising the
 compound and treating an animal having a disease or condition associated
 with forkhead box C2. The compound and methods are useful in diagnosing
 CC and treating developmental disorders e.g. lymphoedemas such as lymphoedema-
 distichiasis, dysgenesis of the mouse iridocorneal angle similar to those
 seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
 CC present sequence is a forkhead box C2 nucleic acid region targeted by the
 CC antisense oligonucleotides.

Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
 DB 15 GCATTGCCACTC 4

RESULT 9
 ID AA226938 standard; DNA; 21 BP.

AA226938;

DT 18-NOV-1999 (first entry)

Human chromosome 11 linked CHD1 gene mutation screening PCR primer #76.

Human; coronary heart disease susceptibility gene; CHD1; mutation;
 chromosome 11; diagnosis; screening; PCR primer; metabolic disorder;
 detection; hypolipidoproteinemia; familial combined hyperlipidaemia;
 insulin resistant syndrome X; multiple metabolic disorder; obesity;
 diabetes; dyslipidaemic hypertension; ss.

Synthetic.

Homo sapiens.

WO945112-A2.

10-SEP-1999.

04-MAR-1999; 99WO-US004682.

04-MAR-1998; 98US-00034941.

06-APR-1998; 98US-0080934P.

(MYRI-) MYRIAD GENETICS INC.

Ballinger DG, Ding W, Wagner S, Hees MA;

WPI; 1999-540844/45.

New isolated coronary heart disease susceptibility gene, used to develop

products for diagnosis and treatment of coronary heart disease and

metabolic disorders.

Example 6; Page 98; 297bp; English.

The present invention describes the human chromosome 11-linked coronary
 heart disease susceptibility gene (CHD1). Mutations in the CHD1 locus in
 the germline are indicative of a predisposition to coronary heart disease
 or to metabolic disorders related to lipid metabolism. Products from the
 CC present invention can be used in the diagnosis of predisposition to
 CC coronary heart disease and to metabolic disorders, including
 hypolipidoproteinemia, familial combined hyperlipidaemia, insulin
 resistant syndrome X or multiple metabolic disorder, obesity, diabetes
 and dyslipidaemic hypertension. CHD1 proteins can be used for treating
 CC coronary heart disease and metabolic disorders. The products can also be
 used for detection and drug screening. AA226932 to AA226841 and AA227027
 CC to AA227029 represent human CHD1 nucleotide sequences. AA227027
 CC AA227026 represent human CHD1 proteins and protein sequences used in the
 CC exemplification of the present invention. AA226842 to AA227014
 CC represent PCR primers used in the screening of mutations in human CHD1;
 CC AA227015 to AA227026 represent oligonucleotides used in the
 CC exemplification of the present invention

Sequence 21 BP; 6 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCA 15
 DB 2 TTGGCACTCCCA 13

RESULT 10
 ID ADS31699 standard; DNA; 22 BP.

ADS31699;

02-DEC-2004 (first entry)

Gene expression inhibition method erbB2 gene PCR primer #10.

KX	cytostatic; gene promoter methylation inducer; cell growth inhibitor;
KM	erbB2 gene expression inhibitor; DNA methylation inducer; dsRNA; CpG;
KW	humat; gene expression; erbB2; tumour; gene transcription; promoter;
KX	small interfering RNA; siRNA; gene silencing; ssr; primer.
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO2004076663-A1.
PD	
XX	10-SEP-2004.
PF	
27-FEB-2004;	2004MO-JP002448.
FR	
27-FEB-2003;	2003US-0449860P.
PA	(NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PI	Taira K, Kawasaki H;
DR	WPI; 2004-662014/64.
PT	
PT	Novel DNA methylation inducer containing double-stranded RNA targeting
PT	region having CpG on DNA in mammalian cell, useful in suppressing gene
PT	expression, and as cell growth inhibitor.
PS	
Example 4;	SEQ ID NO 60; 98bp; Japanese.
CC	The invention relates to a DNA methylation inducer (I) containing double-
CC	stranded (ds) RNA that targets the region which contains CpG or CpNG (N is
CC	A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having
CC	DNA that codes dsRNA that targets the region which contains CpG or CpNG
CC	on DNA in mammalian cell. (I) is useful in the DNA methylation process,
CC	which involves introducing (I) in a mammalian cell, where the mammalian
CC	cell is obtained from human. (II) is useful as gene expression inhibitor
CC	or cell growth inhibitor. A gene expression inhibitor (II) is useful for
CC	suppressing gene expression, where the gene is a disease related gene
CC	relevant to a disease, and the expression of the gene causes the disease.
CC	The gene is erbB2 and the disease is the tumour. (I) is useful for
CC	controlling various biological activities in a mammal by controlling the
CC	transcription level of the respective gene by methylating the respective
CC	DNA. (I) or (II) enables specific methylation of the CpG island-
CC	containing domain on a gene promoter of the target gene, where the
CC	methylation of a promoter suppresses the expression of the target gene.
CC	(I) induces sequence specific DNA methylation in a plant, and controls
CC	the expression of the specific gene at the transcription level. (I)
CC	enables DNA methylation in the promoter region of a gene, where the
CC	methylation changes the structure of the DNA, enabling suppression of the
CC	gene expression at the transcription level (DNA to mRNA). This sequence
CC	corresponds to an erbB2 gene PCR primer used in the method to silence
CC	gene expression in cells.
XX	
Sequence 22 BP;	4 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
QY	
DB	
Query Match	60.0%; Score 12; DB 13; Length 22;
Best Local Similarity	100.0%; Pred. NO. 3.3e+03;
Matches 12;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	
4 TTGCCACTCCCA 15	
13 TTGCCACTCCCA 2	
ID	
AB183921	
ID	AB183921 standard; DNA; 24 BP.
AC	
AB183921;	
DT	
15-FEB-2002	(first entry)
DE	Capture oligonucleotide zip IH#762 oligo #2.

XX	
XX	
XX	Human; K-raas; PCR primer; probe; capture probe; mutation detection;
KM	lipase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KM	infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KM	oncogene; tumour suppressor; human papillomavirus; forensic;
KM	environmental monitoring; food industry; feed industry; ss.
XX	
OS	Synthetic.
XX	
PN	WO200179548-A2.
XX	
PD	25-OCT-2001.
XX	
PF	04-APR-2001; 2001WO-US010958.
XX	
PR	14-APR-2000; 2000US-0197271P.
XX	
PA	(CORR) CORNELL RES FOUND INC.
XX	
PI	Barany F, Zivvi M, Gerry NP, Favis R, Kliman R,
XX	
PT	WPI; 2002-034366/04.
XX	
XX	
XX	Designing capture oligonucleotide probes for use on a support to which
XX	complementary oligonucleotides hybridize with little mismatch.
XX	

Example 5; Flg 25; 300pp; English.

CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BCL1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting complimentary scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying (if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention

Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

Query Match	60.0%;	Score 12;	DB 6;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 3.3e+03;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	

OY		1	GCATTGCCACTC	12
Dd		6	GCATTGCCACTC	17

DE	Capture oligonucleotide zip ID#762 oligo #1
XX	
XX	15-FEB-2002 (first entry)
XX	
XX	ABI83920;
XX	
XX	ABI83920 standard; DNA; 24 BP.
ID	ABI83920/c
RESULT 12	

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KM ligation detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KM oncogene; tumour suppressor; human papillomavirus; forensic;
KM environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PI (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivri M, Gerry NP, Favls R, Klman R;
XX WPI; 2002-034366/04.
DR
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC mediasi. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB19746 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
XX
Query Match 60.0%; Score 12; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCATTGCCACTC 12
Db 19 GCATTGCCACTC 8
XX
RESULT 13
ABSS59154 ID ABSS59154 standard; DNA; 26 BP.
XX
XX AC ABSS59154;
XX
XX 05-NOV-2002 (first entry)
DT
XX Human G-protein coupled receptor, probe #101.

XX Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KM diabetes; cell signal processing; metabolic pathway modulation; cancer;
KM adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KM immune response; neurodegenerative disorder; inflammatory disorder;
KM Crohn's disease; multiple sclerosis; Albritght hereditary osteodystrophy;
KM probe; ss.
XX
OS Homo sapiens.
XX
PN WO200259313-A2.
XX
PD 01-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049394.
XX
PR 18-DEC-2000; 2000US-0256635P.
XX
PR 21-DEC-2000; 2000US-0257876P.
XX
PR 04-JAN-2001; 2001US-0259743P.
XX
PR 10-JAN-2001; 2001US-0260718P.
XX
PR 12-JAN-2001; 2001US-0261498P.
XX
PR 24-JAN-2001; 2001US-0263689P.
XX
PR 08-FEB-2001; 2001US-0267464P.
XX
PR 22-FEB-2001; 2001US-0271021P.
XX
PR 14-MAR-2001; 2001US-0275946P.
XX
PR 23-MAR-2001; 2001US-0278150P.
XX
PR 18-APR-2001; 2001US-0284591P.
XX
PR 23-APR-2001; 2001US-0285718P.
XX
PR 19-JUN-2001; 2001US-0299327P.
XX
PR 16-AUG-2001; 2001US-0312902P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Gaman SJ, Vermet CAM, Shenoy SG, Gusev V, Malyanekar UM, Edinger S;
PI Gerlach V, Smithson G, Stone DJ, Sciorio P, Macdougall JR, Gunther B;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX WPI; 2002-599789/64.
DR
XX
PT New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
PS Claim 9; Page 568; 685pp; English.
XX
CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albritght hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. ABSS8747-ABSS9231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
SQ Sequence 26 BP; 7 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 60.0%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTGCCACTCCCA 15
 Db 5 TTGCCACTCCCA 16
 RESULT 14
 AB088545 standard; DNA; 26 BP.
 AC AB088545;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human GPCR probe SEQ ID NO:257.
 XX
 KW Human; G protein coupled receptor; GPCR; GPCR; neuroprotective;
 KW neurotrophic; anti-HIV; antidiabetic; antidiabetic; anorectic; haemostatic;
 KW immunomodulator; anti-inflammatory; antidiabetic; anorectic; haemostatic;
 KW antibacterial; fungicide; protozoal; virucide; nephrotoxic; osteopathic;
 KW cardiant; antitumor; antidiabetic; hepatocytic; antiparkinsonian; HIV;
 KW vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes;
 KW metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma;
 KW infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer;
 KW allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder;
 KW systemic lupus erythematosus; probe; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200250276-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 18-DEC-2001; 2001WO-US049347.
 XX
 PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261988P.
 PR 24-JAN-2001; 2001US-0263689P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-028150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-029327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Li L, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P,
 PI Smithson G, Payman JA, Macdougall JR, Vernet CM, Shenoy S,
 PI Gunther E, Miller I, Tchenev VT, Anderson D, Gusev V, Malankar UM;
 PI Zhong H, Ellemann KE, Wolenc A;
 XX
 DR WPI; 2002-557660/59.
 XX
 PT New isolated human G-protein coupled receptor X (GPCRX) polypeptide,
 PT useful for treating or preventing GPCR-associated disorders e.g.
 PT diabetes, atherosclerosis, cancer or obesity.
 XX
 PS Example 3; Page 245; 354pp; English.
 XX
 CC AB088354 to AB088417 represent human G protein coupled receptor (GPCR)
 CC cDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins
 CC from the present invention. GPCR sequences can have neuroprotective,
 CC neurotrophic, anti-HIV, antiaesthetic, antiatherosclerotic, cyostatic,
 CC immunomodulator, anti-inflammatory, antidiabetic, anorectic, haemostatic,
 CC antibacterial, fungicide, protozoal, virucide, nephrotoxic, osteopathic,
 CC cardiant, antitumor, antidiabetic, hepatocytic and antiparkinsonian

CC activities, and can be used in vaccines and gene therapy. GPCR proteins,
 CC nucleic acid molecules, and antibodies from the present invention can be
 CC used for manufacturing a medicament for treating or preventing a GPCR-
 CC associated disorder or syndrome related to cell signal processing and
 CC metabolic pathway modulation, such as cardiomyopathy, atherosclerosis,
 CC diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or
 CC viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease,
 CC ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus
 CC erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be
 CC used diagnostically to monitor protein levels in tissues as part of a
 CC clinical testing procedure such as in determining the efficacy of a given
 CC treatment regimen. AB088418 to AB088639 represent PCR primers and probes
 CC for the human GPCRs of the present invention
 XX
 SQ Sequence 26 BP; 7 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred.No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 TTGCCACTCCCA 15
 Db 5 TTGCCACTCCCA 16
 RESULT 15
 AD104496
 ID AD104496 standard; DNA; 26 BP.
 XX
 AC AD104496;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human G-protein coupled receptor forward primer #43.
 XX
 KW ss; primer; PCR; human; G-protein coupled receptor; GPCR; cancer;
 KW breast; ovarian cancer; hypercalcaemia; endometriosis; Crohn's disease;
 KW appendicitis; cirrhosis; infertility; cardiovascular disorder;
 KW cardiomyopathy; atherosclerosis; autoimmune disease; scleroderma;
 KW systemic lupus erythematosus; diabetes; pancreatitis;
 KW Alzheimer's disease; stroke; myasthenia gravis; schizophrenia;
 KW renal disorder; glomerulonephritis; renal tubular acidosis; immunogen;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003198955-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 19-DEC-2001; 2001US-00025806.
 XX
 PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261988P.
 PR 24-JAN-2001; 2001US-0263689P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-028150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-029327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (LIL/) LI L.
 PA (PADI/) PADIGARU M.
 PA (BAL/) BALLINGER R A.
 PA (KEKU/) KEKUDA R.
 PA (COLM/) COLMAN S D.
 PA (SPY/) SPYTEK K A.

PA (CASM/) CASMAN S J.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (SCIO/) SCIORE P.
 PA (SMIT/) SMITHSON G.
 PA (PEYM/) PEYMAN J A.
 PA (MACD/) MACDOUGALL J R.
 PA (STON/) STONE D J.
 PA (VERN/) VERNET C A M.
 PA (SHEN/) SHENOY S G.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (TCHE/) TCHERNEV V T.
 PA (ANDE/) ANDERSON D W.
 PA (GUSE/) GUSEV V Y.
 PA (MALY/) MALYANKAR U M.
 PA (ZHON/) ZHONG H.
 PA (ELLE/) ELLERMAN K.
 PA (WOLE/) WOLENC A R.
 XX
 PI I L Padigaru M, Ballinger RA, Kekuda R, Colman SD, Spytek KA,
 PI Casman SJ, Edinger SR, Gerlach V, Sciore P, Smithson G, Peyman JA,
 PI Macdougall JR, Stone DJ, Vernet CM, Shenoy SG, Gunther E, Millet I,
 PI Tcherev VT, Anderson DW, Gusev VY, Malyankar UM, Zhong H;
 PI Ellerman K, Wolenc AR;
 XX
 DR WPI; 2003-852781/79.
 XX
 PT New isolated GPCRX polypeptide, useful for determining the predisposition
 PT to or presence of GPCRX-associated disorders or conditions, and in
 PT manufacturing a medicament for treating or preventing diseases such as
 PT cancer and diabetes.
 XX
 PS Example 3; SEQ ID NO 257; 221bp; English.
 PS
 CC The invention relates to an isolated G-protein coupled receptor (GPCRX)
 CC polypeptide. The polypeptide, nucleic acid, antibody, and their
 CC biologically active derivatives or fragments, are useful in determining
 CC the predisposition to or presence of GPCRX-associated disorders or
 CC syndromes and in manufacturing a medicament for treating, diagnosing or
 CC preventing the said disorders such as cancer (e.g. breast or ovarian
 CC cancers), hypercalcaemia, endometriosis, Crohn's disease, appendicitis,
 CC cirrhosis, infertility, cardiovascular disorders (e.g. cardiomyopathy,
 CC atherosclerosis), autoimmune diseases (e.g. scleroderma, systemic lupus
 CC erythematosus), diabetes, pancreatitis, Alzheimer's disease, stroke,
 CC myasthenia gravis, schizophrenia, renal disorders (e.g.
 CC glomerulonephritis, renal tubular acidosis), and/or other similar
 CC pathologies and disorders. The polypeptides are also useful as immunogens
 CC to produce antibodies and as vaccines. The present sequence represents a
 CC GPCR primer of the present invention.
 CC
 XX
 SQ Sequence 26 BP; 7 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 60.0%; Score 12; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTGCCACTCCCA 15
 DB 5 TTGCCACTCCCA 16
 DB
 RESULT 16
 AAV44981/C
 ID AAV44981 standard; cDNA; 29 BP.
 XX
 AC AAV44981;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE PCR primer for UCP2 gene transcriptional promoter sequence.
 XX
 KW Uncoupling protein 2; UCP2 gene; transcriptional promoter; mouse;

KW mitochondrial protein; cis transcriptional regulatory activity; therapy;
 KW expression modulator screening; fat feeding; diabetes; obesity;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5807740-A.
 XX
 PD 15-SEP-1998.
 XX
 PF 25-APR-1997; 97US-00846012.
 XX
 PR 25-APR-1997; 97US-00846012.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Chen J, Amaral MC;
 XX
 DR WPI; 1998-520130/44.
 XX
 PT Mouse UCP2 gene promoter - useful for forming transfected cell lines
 PT employed in drug screening assays.
 XX
 PS Example; Col 4; 9pp; English.
 PS
 CC This sequence is a PCR primer for the human mitochondrial uncoupling
 CC protein 2 (UCP2) gene transcriptional promoter of the invention. The
 CC promoter has cis transcriptional regulatory activity. Cells containing
 CC the promoter attached to a non-UCP2 gene, in which the non-UCP2 gene is a
 CC reporter gene can be used in screening assays for modulators of UCP2 gene
 CC expression, which may be useful for treating disorders in which the UCP2
 CC gene is upregulated in response to fat feeding, e.g. diabetes and obesity
 CC
 XX
 SQ Sequence 29 BP; 7 A; 5 C; 13 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 60.0%; Score 12; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTGCCACTCCCA 15
 DB 20 TTGCCACTCCCA 9
 DB
 RESULT 17
 AAV08886/C
 ID AAV08886 standard; cDNA; 29 BP.
 XX
 AC AAV08886;
 XX
 DT 20-MAR-2003 (revised)
 DT 25-FEB-1999 (first entry)
 XX
 DE PCR primer for UCP2 promoter.
 XX
 KW UCP2; promoter; transcription factor; modulator; diabetes; obesity;
 KW therapy; PCR primer; ds.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5849514-A.
 XX
 PD 15-DEC-1998.
 XX
 PF 19-JUN-1998; 98US-00100297.
 XX
 PR 25-APR-1997; 97US-00846012.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Chen J, Amaral MC;

XX WPI; 1999-069722/06.

XX Screening assay for modulators of UCP2 gene expression - based on
PT Interaction of transcription factor and defined UCP2 promoter sequence.
XX

PS Example; Col 4; 9pp; English.

CC This sequence represents a PCR primer for the UCP2 promoter. The
CC amplified sequence is used in the method of the invention, which is a
CC screening assay for agents that modulate the effect of a transcription
CC factor on a UCP2 promoter comprising combining the promoter and
CC transcription factor in the presence and absence of a candidate agent and
CC determining any change in the effect of the transcription factor on the
CC promoter. The promoter comprises at least 50 nucleotides of a sequence
CC comprising nucleotides 1-460 of the UCP2 promoter (see AAV0879). The
CC method is used to identify agents that modulate UCP2 gene transcription
CC (agents that upregulate UCP2 are potentially useful for treating diabetes
CC and obesity). (Updated on 20-MAR-2003 to correct PF field.)
XX

SQ Sequence 29 BP; 7 A; 5 C; 13 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 60.0%; Score 12; DB 2; Length 29;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTGCCA 15

DB 20 TTGCCACTGCCA 9

RESULT 18

AAZ28769/C

ID AAZ28769 standard; DNA; 39 BP.

AC AAZ28769;

DT 01-FEB-2000 (first entry)

DE G-less oligonucleotide GLESS7.

KM Oligonucleotide; capture assay; tat; modulation; transcription; guanine;

KW mRNA expression; activator; inhibitor; detection; ss; gene expression;

XX antineoplastic; antifungal; antiviral; disease.

OS Synthetic.

XX W09950459-A2.

PD 07-OCT-1999.

PF 31-MAR-1999; 99WO-US007127.

PR 31-MAR-1998; 98US-00052995.

XX (TULA-) TULARIK INC.

PA Sivara M, Strulovici B, Flores OA;

PI WPI; 1999-610868/52.

PT A new method for detecting RNA in a sample.

PS Example I; Page 40; 60pp; English.

CC The oligonucleotides AAZ28763-228772 are used in a capture assay for Tat-
CC modulated transcription of guanine (G)-less mRNA expression in vitro,
CC following addition of a potential transcriptional activator or inhibitor.
CC The method is used to detect a selected RNA in a sample, comprising: (a)
CC contacting a sample with an oligonucleotide comprising a region
CC complementary to the selected RNA to form an RNA/DNA duplex, (b) cleaving
CC single-stranded RNA in the sample, (c) binding RNA duplex to a
CC recognition reagent immobilized on a solid substrate, and (d) detecting

CC bound RNA duplex. The invention is used as a high throughput assay to
CC identify modulators of gene expression that may serve for example as
CC antineoplastic, antifungal or antiviral agents for the treatment of a
CC wide variety of diseases
XX

SQ Sequence 39 BP; 16 A; 0 C; 19 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 60.0%; Score 12; DB 2; Length 39;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCATTCT 19

DB 27 CACTCCATTCT 16

RESULT 19

AAI55696/C

ID AAI55696 standard; DNA; 41 BP.

AC AAI55696;

DT 04-DEC-2003 (first entry)

DE Human zinc finger 32-56-related probe #1.

KW Human; zinc finger 32.56; cancer; HIV; probe; ss.

OS Homo sapiens.

XX CN1381467-A.

PD 27-NOV-2002.

PF 18-APR-2001; 2001CN-00112608.

PR 18-APR-2001; 2001CN-00112608.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2003-249003/25.

PT New Polypeptide-human zinc finger protein-32.56, encoding polynucleotide,
PT antagonist and recombinant production, useful for treating cancer and
PT HIV.

PS Example 7; Page 22; 0pp; Chinese.

CC The invention relates to a novel human zinc finger 32.56 polypeptide, the
CC encoding polynucleotide, an antagonist and a method for recombinant
CC production. The polypeptide is useful for treating cancer and HIV
CC infection. The current sequence is that of the human zinc finger 32.56-
CC related probe #1
XX

SQ Sequence 41 BP; 10 A; 7 C; 10 G; 14 T; 0 U; 0 Other;

Query Match

Best Local Similarity 60.0%; Score 12; DB 10; Length 41;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCATTCT 20

DB 27 ACTCCATTCT 16

RESULT 20

AAI75760/C

ID AAI75760 standard; DNA; 51 BP.

AC AAI75760;

DT 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ:2701.
DB
XX
OS Homo sapiens.
XX
XX MO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX
XX Shimkete RA, Leach M;
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 877; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 10 A; 12 C; 16 G; 13 T; 0 U; 0 Other;
QY
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 5 TGCCACTCCCAT 16
35 TGCCACTCCCAT 24

RESULT 21
AA175759/c
ID AA175759 standard; DNA; 51 BP.
XX
XX AA175759;
XX
DT 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:2700.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX MO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX
XX Shimkete RA, Leach M;
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 877; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 14 A; 9 C; 15 G; 13 T; 0 U; 0 Other;
QY
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 5 TGCCACTCCCAT 16
45 TGCCACTCCCAT 34

KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX MO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX
XX Shimkete RA, Leach M;
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 877; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 14 A; 9 C; 15 G; 13 T; 0 U; 0 Other;
QY
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 5 TGCCACTCCCAT 16
45 TGCCACTCCCAT 34

RESULT 22
AA175758/c
ID AA175758 standard; DNA; 51 BP.
XX
XX AA175758;
XX
DT 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:2699.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX MO200140521-A2.
XX

PD 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
PR 30-NOV-1999; 99US-0168138P.
FR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M,
XX WPI; 2001-356160/37.
DR
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX
PS Claim 1; Page 877; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AA153114 to AA153329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC deletions, (1) may be used to treat disorders by rectifying mutations or
CC by expressing inactive proteins or to supplement the activity of polypeptides
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
SQ
Sequence 51 BP; 13 A; 9 C; 16 G; 13 T; 0 U; 0 Other;
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGCCACTGCCAT 16
DB 45 TGCCACTGCCAT 34
RESULT 23
AAH38540
ID AAH38540 standard; DNA; 51 BP.
XX
AC AAH38540;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 1336.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.
XX
OS Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
PD 13-OCT-2000; 2000WO-US028436.
PF

XX
XX 15-OCT-1999; 99US-0160096P.
PR
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX
XX Picoult-Newburg L, Pohl M;
PI
XX
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
PS Claim 1; Page 56; 83pp; English.
XX
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism
SQ
Sequence 51 BP; 12 A; 16 C; 14 G; 9 T; 0 U; 0 Other;
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCATC 12
DB 28 GCATTGCCATC 39
RESULT 24
ABL00487/C
ID ABL00487 standard; DNA; 51 BP.
XX
AC ABL00487;
XX
XX 05-MAR-2002 (first entry)
XX
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:478.
DE
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antitubercular;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX
XX
XX Homo sapiens.
XX
XX WO200138586-A2.
XX
XX 31-MAY-2001.
XX
PD 22-NOV-2000; 2000WO-US032311.
PF
XX

PR 24-NOV-1999; 99US-0167383P.
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX WPI; 2001-355949/37.
DR
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
XX Claim 1; Page 392; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterized
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
XX Sequence 51 BP; 12 A; 11 C; 15 G; 13 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 12; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTC 12
Db 27 GCATTGCCACTC 16
RESULT 25
ABN44520
ID ABN44520 standard; DNA; 60 BP.
XX
XX ABN44520;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:17268.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX W0200210449-A2.
PN
XX
XX 07-FEB-2002.
PD
XX 20-JUL-2001; 2001WO-IB001903.
PF
XX 28-JUL-2000; 2000US-0221607P.
PR
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX WPI; 2002-257383/30.
DR
XX

PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 17268; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC a specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 60 BP; 11 A; 17 C; 13 G; 19 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 12; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTC 12
Db 44 GCATTGCCACTC 55
RESULT 26
ABN42321/c
ID ABN42321 standard; DNA; 60 BP.
XX
XX ABN42321;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:15069.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX W0200210449-A2.
PN
XX
XX 07-FEB-2002.
PD
XX 20-JUL-2001; 2001WO-IB001903.
PF
XX 28-JUL-2000; 2000US-0221607P.
PR
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX WPI; 2002-257383/30.
DR
XX New oligonucleotide libraries comprising oligonucleotides which
PT

designed to detect single-nucleotide polymorphisms useful for diagnosis and cell typing, is

acid (pNA) oligomers describes novel oligonucleotide primers or peptide nucleic acid (pNA) oligomers for detecting single nucleotide polymorphisms (SNPs) and cytosine methylation status in chemically altered/pre-treated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. The oligomers are also used for detecting cell cycle differentiation. The oligomers represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 CTCCTCATTTCT 20
 |||||
 11 CTCCTCATTTCT 1

RESULT 29

ABCI4054/C
 ID ABCI4054 standard; DNA; 13 BP.

XX ABCI4054;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO-14061 for detecting SNP TSC0003215.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 14061; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 ACTGCCATTCT 19
 |||||

Db 13 ACTGCCATTCT 3

RESULT 30

ABCI4055
 ID ABCI4055 standard; DNA; 13 BP.

XX ABCI4055;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 14062 for detecting SNP TSC0003215.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 14062; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 ACTGCCATTCT 19
 |||||
 Db 1 ACTGCCATTCT 11

RESULT 31

AAV95069
 ID AAV95069 standard; RNA; 17 BP.

XX AAV95069;

XX 24-FEB-1999 (first entry)

DE Canine IL-2 receptor g-chain substrate position 17.

XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;

KM hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KM autoimmune disease; psoriasis; allergy; inflammatory disease;
KM graft rejection; ss.
XX
OS Synthetic.
OS Canis sp.
XX
PN WO9824913-A2.
PD
XX 11-JUN-1998.
XX
XX 02-DEC-1997; 97WO-US021748.
XX
PR 03-DEC-1996; 96US-00759306.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Mcswigen JA;
XX
XX WPI; 1998-33332/29.
DR
XX
XX
PT Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,
PT autoimmune disease and allergies.
XX
XX Claim 4; Page 45; 61pp; English.
XX
XX The present sequence invention describes ribozymes targeted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and
CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
SQ Sequence 17 BP; 4 A; 8 C; 2 G; 0 T; 3 U; 0 Other;
Query Match 55.0%; Score 11; DB 2; Length 17;
Best Local Similarity 72.7%; Pred. No. 1.2e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATGCCACTC 12
Db 6 CAUUGCCACCTC 16
RESULT 32
ABA95013/c
ID ABA95013 standard; DNA; 18 BP.
XX
XX ABA95013;
AC
XX
DT 11-SEP-2003 (revised)
DT 21-MAY-2002 (first entry)
XX
XX ISAV structural protein-1 (SP-1) forward primer.
DE
XX
XX Structural protein-1; SP-1; infectious salmon anaemia virus; ISAV;
KM infectious salmon anaemia; ISA; vaccine; virucide; fish; PCR primer; ss.
XX
OS Infectious salmon anemia virus.
XX
XX
XX EP1094069-A1.
XX
XX 25-APR-2001.
PD
XX
XX 12-OCT-2000; 2000EP-00203555.
PF
XX
PR 18-OCT-1999; 99EP-00203401.
XX
XX (ALKU) AKZO NOBEL NV.
PA
XX
PI Biering E, Krossoy B;

XX
DR WPI; 2001-487577/29.
XX
XX
PT New polynucleotide encoding structural protein-1 of infectious salmon
PT anemia virus in vaccine preparation for protecting fish against the viral
PT infection, and in diagnostics.
XX
XX Disclosure; Page 5; 24pp; English.
XX
XX
XX The invention relates to a structural protein-1 (SP-1) of infectious
CC salmon anaemia virus (ISAV). The SP-1 polynucleotide, protein or specific
CC antibodies are useful in diagnostics, and in vaccines to protect fish
CC against infection with ISAV. The SP-1 polynucleotide is useful for
CC producing vector vaccines against the virus, and for recombinant
CC production of SP-1, substantially free from other ISA viral protein. The
CC present sequence represents an oligonucleotide derived from the ISAV SP-1
CC DNA, that can be used as a primer. (Updated on 11-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 18 BP; 3 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 55.0%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGCACCTCCCA 15
Db 15 TGCACCTCCCA 5
RESULT 33
ABA93931/c
ID ABA93931 standard; DNA; 18 BP.
XX
XX ABA93931;
AC
XX
DT 04-JUN-2003 (first entry)
DT
XX
XX pCDNA3 vector polylinker PCR primer.
DE
XX
XX Human; androgen receptor; AR; cytostatic; androgen receptor inhibitor;
KM gene therapy; ribozyme; cell proliferation; prostatic cancer cell;
KM prostate hyperplasia; prostate cancer; androgen dependent pathology; ss;
KM hammerhead ribozyme; HR2; PCR; primer; polylinker; pCDNA3.
XX
XX
OS Synthetic.
XX
XX US6489163-B1.
XX
XX 03-DEC-2002.
PD
XX
XX 08-MAY-1997; 97US-00853164.
XX
XX 08-MAY-1996; 96US-0016590P.
PR
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX
XX Roy AK, Chen S;
PI
XX
XX WPI; 2003-352114/33.
DR
XX
XX
XX New synthetic ribozyme that cleaves androgen receptor mRNA, useful for
PT treating prostate hyperplasia or cancer, and other androgen dependent
PT pathologies.
XX
XX
PS Disclosure; Col 6; 38pp; English.
XX
XX The invention describes a synthetic ribozyme (I) that cleaves androgen
CC receptor mRNA. A vector comprising (I) is useful for reducing androgen
CC receptor activity in cultured prostate cells, by providing to the cells a
CC preparation comprising the vector. The vector is also useful for
CC inhibiting the proliferation of prostatic cancer cells in vitro, by
CC providing the vector expressing (I) to the cells. (I) is useful for

CC treating prostate hyperplasia or cancer, and other androgen dependent
CC pathologies. This sequence represents a primer used to detect expression
CC of hammerhead ribozyme HR2 in cultured cells
XX
SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
DB 13 TGGCACTCCCA 3

RESULT 34
ADA61988/C
ID ADA61988 standard; DNA; 18 BP.

AC ADA61988;

DT 20-NOV-2003 (first entry)

DE Vector pCDNA3 RT-PCR primer.

XX Cytostatic; ss; androgen receptor; ribozyme; prostatic hyperplasia;
KM prostate cancer; PCR; primer; RT-PCR; reverse transcriptase PCR; pCDNA3.

OS Synthetic.

PN US2003077639-A1.

PD 24-APR-2003.

PF 17-SEP-2002; 2002US-00246078.

PR 08-MAY-1996; 96US-0016590P.

PR 08-MAY-1997; 97US-00853164.

XX (TEXA) UNIV TEXAS SYSTEM.

PA Roy AK, Chen S;

PI WPI; 2003-615997/58.

DR New synthetic ribozyme capable of selectively targeting androgen receptor
PT mRNA, useful in inactivating androgen receptor gene expression, and for
PT treating prostate hyperplasia.

PS Disclosure; Page 7; 40pp; English.

XX The invention relates to synthetic ribozyme capable of selectively
CC targeting the androgen receptor mRNA. Also included are a gene encoding
CC the synthetic ribozyme, a vector comprising the gene (where expression of
CC the gene in a human prostatic cancer cell is capable of inhibiting
CC androgen receptor activation), reducing androgen receptor activity in an
CC animal having prostatic hyperplasia by administering a preparation
CC comprising the vector, and treating prostatic hyperplasia by
CC administering to the patient a formulation of an active preparation of a
CC ribozyme gene construct comprising a human promoter sequence in a vector
CC carrier (where the ribozyme gene construct comprises a ribozyme gene that
CC provides an expression product capable of selectively reducing androgen
CC receptor activation). The synthetic ribozyme is capable of selectively
CC targeting androgen receptor mRNA and can be used in the inactivation of
CC androgen receptor gene expression, and for treating prostatic hyperplasia
CC and prostate cancer. The present sequence is reverse transcriptase (RT)-
CC PCR primer used to assess ribozyme expression in transfected cells,
CC designed against the vector pCDNA3.

SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
DB 13 TGGCACTCCCA 3

RESULT 35
AAV18643
ID AAV18643 standard; DNA; 19 BP.

AC AAV18643;

DT 21-JUL-1998 (first entry)

DE Homo sapiens BAP-1 PCR primer.

XX BRCAL associated; BAP-1; breast cancer; ovarian cancer;
KM breast and ovarian cancer susceptibility gene; diagnosis;
KM ubiquitin carboxy-terminal hydrolase; activity; ss.

OS Synthetic.

PN W09805968-A1.

PD 12-FEB-1998.

PF 30-JUL-1997; 97WO-US013684.

PR 02-AUG-1996; 96US-0022997P.

PR 19-FEB-1997; 97US-0038109P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PA Rauscher FJ, Jensen DE;

PI WPI; 1998-145723/13.

DR DNA encoding mammalian BRCAL associated protein, BAP-1 - useful for, e.g.
PT detecting cancer involving breast and ovarian cancer susceptibility gene
PT BRCAL.

PS Example 8; Page 45; 100pp; English.

XX The sequence is that of a PCR primer which was used in the mutational
CC analysis of BAP-1 (BRCAL associated protein) cDNA
CC
SQ Sequence 19 BP; 4 A; 10 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCAATT 17
DB 6 CCACTCCCAATT 16

RESULT 36
AAV80303/C

ID AAV80303 standard; DNA; 20 BP.

AC AAV80303;

DT 16-FEB-1999 (first entry)

DE Murine GILR cDNA specific reverse primer.

XX Glucocorticoid-induced leucine-zipper family related protein; GILR;
KM apoptosis; lymphocyte; recombinant; medicament; Fas-Ligand; AIDS;
KM CD3/T cell receptor; TCR; intracellular mediator; treatment; tumour;
KM inflammation; acute hepatitis; autoimmune disease; diabetes; mouse;
KM multiple sclerosis; graft rejection; immunodeficiency; HIV; detection;

KW diagnosis; RNase protection analysis; RPA; PCR primer; ss.
 XX Synthetic.
 OS Mus sp.
 XX WO9849291-A1.
 XX PD 05-NOV-1998.
 XX PF 27-APR-1998; 98WO-EP002490.
 XX PR 28-APR-1997; 97EP-00107033.
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX Ricciardi C;
 XX PI WPI; 1999-009422/01.
 XX DR
 XX PT New isolated glucocorticoid-induced leucine-zipper family protein - used
 PT to develop products for modulating apoptosis and lymphocyte activity for
 PT treating, e.g. inflammation, autoimmune diseases, tumours or HIV
 PT infection.
 XX
 XX PS Example 1; Page 55; 109pp; English.
 XX
 CC Sequences AAV80302 and AAV80303 represent primers specific for
 CC glucocorticoid-induced leucine-zipper family related (GILR) protein
 CC protection cDNA. These were used for constructing a probe for the RNase
 CC protection analysis (RPA). The GILR protein, isoform, fragments or
 CC analogues of the protein are capable of inhibiting apoptosis and
 CC stimulating lymphocyte activity. Eukaryotic or prokaryotic host cells
 CC transformed with an expression vector containing the GILR encoding
 CC nucleic acid can be used to produce the protein recombinantly. The mouse
 CC and human GILR proteins, isoforms, analogues, fragments or derivatives or
 CC DNA encoding them can be used for the manufacture of a medicament for the
 CC inhibition of apoptosis in cells mediated by the Fas-Ligand system, CD3/T
 CC cell receptor (TCR) system or other intracellular mediators of apoptosis.
 CC They can be used for treating inflammation, acute hepatitis, autoimmune
 CC diseases, graft rejection, diabetes, multiple sclerosis, AIDS or
 CC immunodeficiencies. Inhibition of the activity of GILR proteins in cells
 CC can be used for enhancing apoptosis in cells. Such inhibition can be used
 CC for the treatment of tumour cells or HIV-infected cells or other diseased
 CC cells. The products can also be used for detection and diagnostic
 CC applications
 CC
 CC SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
 CC
 CC Query Match 55.0%; Score 11; DB 2; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 5 TGGCACTCCCA 15
 CC Db 18 TGGCACTCCCA 8
 CC
 CC RESULT 37
 CC AAA29200
 CC ID AAA29200 standard; DNA; 20 BP.
 CC XX
 CC AC AAA29200;
 CC XX
 CC DT 12-SEP-2000 (first entry)
 CC XX
 CC DE Sense primer for hVR3 3' DNA amplification.
 CC XX
 CC KW hVR3; vanilloid receptor; dorsal root ganglia; chromosome 12; capsaicin;
 KW marker D128177E; marker D1281893; nociceptor; calcium influx; inhibitor;
 KW modulator; analgesic; uteropathic; anti-rheumatic; anti-arthritis;
 KW neuropathic; cerebroprotective; vasotropic; anti-asthmatic;
 KW anti-inflammatory; anti-migraine; primer; ss.
 XX

OS Homo sapiens.
 XX EN WO200032766-A1.
 XX PD 08-JUN-2000.
 XX PF 30-NOV-1999; 99WO-EP00284.
 XX PR 01-DEC-1998; 98GB-00026359.
 XX (GLAX) GLAXO GROUP LTD.
 XX PA
 XX PI Delany NS, Sanson P, Tate SN;
 XX XX WPI; 2000-412315/35.
 XX DR
 XX PT Human vanilloid receptor protein or its variant useful for treating or
 PT preventing a disorder responsive to the modulation of hVR activity, such
 PT as pain, neuropathies, neuralgia, algnesia, neurodegeneration.
 XX
 XX PS Example 9; Page 28; 135pp; English.
 XX
 CC Human VR1 is preferentially expressed in human dorsal root ganglia (DRG)
 CC and relative to hVR3 has the highest sequence homology with the rat VR1.
 CC The hVR3 gene maps to chromosome 12 near markers D128177E and D1281893.
 CC hVR1 is activated by capsaicin, the irritant in hot peppers. VRs are
 CC nociceptors, transmitting nociceptive and thermosensitive pain information
 CC back to pain-processing centres in the central nervous system. They are
 CC also sites for the release of pro-inflammatory mediators in the
 CC periphery. Capsaicin induces a flux of cations in DRG. The actions of
 CC capsaicin (excitation/desensitisation) are mediated by VRs. The natural
 CC ligand of the recently identified rat VR1 is unknown. It is possible that
 CC hVR sub-types may provide targets for the development of novel analgesic
 CC agents and agents which may interact with other disorders. hVR is useful
 CC for treatment or prophylaxis of a disorder responsive to the modulation
 CC of hVR activity, e.g. pain, neuropathic pain, inflammatory pain, chronic
 CC pain, post-operative pain, rheumatoid arthritis, neuropathies,
 CC neuralgia, algnesia, neurodegeneration, nerve injury, stroke, ischaemia,
 CC migraine, irritable bowel syndrome (IBS), a respiratory disorder, asthma,
 CC chronic obstructive pulmonary disease (COPD), urological disorder,
 CC neuropathy, incontinence, interstitial cystitis or an inflammatory
 CC disorder in a human patient (claimed)
 CC
 CC SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
 CC
 CC Query Match 55.0%; Score 11; DB 3; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 10 CTCGCATTCTT 20
 CC Db 5 CTCGCATTCTT 15
 CC
 CC RESULT 38
 CC ADA74107
 CC ID ADA74107 standard; DNA; 20 BP.
 CC XX
 CC AC ADA74107;
 CC XX
 CC DT 20-NOV-2003 (first entry)
 CC XX
 CC DE Equine laminin gamma-2 cDNA PCR primer #16.
 CC XX
 CC KW Horse; PCR; ss; laminin gamma-2; junctional epidermolysis bullosa; JEB;
 KW primer.
 XX
 XX OS Equus caballus.
 XX OS US2003143545-A1.
 XX PN 31-JUL-2003.
 XX PD

PF 24-JAN-2002; 2002US-00053662.
 XX
 PR 24-JAN-2002; 2002US-00053662.
 XX
 PA (BAIR/) BAIRD J.
 PA (LIND/) LINDER K.
 PA (MENE/) MENEGUZZI G.
 PA (SPIR/) SPIRITO F.
 PA (CHAR/) CHARLESWORTH A.
 XX
 PI Baird J, Linder K, Meneguzzi G, Spirito F, Charlesworth A;
 DR WPI; 2003-626651/59.
 XX
 PT New isolated equine laminin gamma-2 polypeptide and encoding
 PT polynucleotide, useful for diagnosing junctional epidermolysis bullosa in
 PT horses.
 PS
 PS Example 2; Page 5; 34pp; English.
 XX
 CC The invention relates to the equine laminin gamma-2 polypeptide and the
 CC polynucleotide encoding it. The invention also relates to a method for
 CC diagnosing junctional epidermolysis bullosa (JEB) in a horse, comprising
 CC obtaining a biological sample from the horse, isolating DNA and
 CC amplifying the DNA encoding laminin gamma-2 using appropriate primers and
 CC analysing the amplified nucleic acid to identify the presence of a
 CC mutation, where the homozygous presence of the mutated nucleic acid
 CC encoding laminin gamma-2 indicates the presence of epidermolysis bullosa.
 CC Alternatively, the protein component from the sample can be isolated and
 CC screened for laminin gamma-2, where the absence of laminin gamma-2
 CC polypeptide indicates the presence of JEB. The laminin gamma-2 nucleic
 CC acid, proteins and antibodies against the proteins are useful for
 CC diagnosing JEB in horses. This sequence represents a PCR primer used to
 CC amplify cDNA encoding equine laminin gamma-2.
 XX
 XX Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 55.0%; Score 11; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CTCGCATTCTT 20
 DB 7 CTCGCATTCTT 17
 AC
 AC ADI57250;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Major allergenic storage protein FAGAG1 PCR primer FAG22 SEQ ID NO:9.
 KW food testing; allergen; PCR primer; Fagopyrum esculentum;
 KW major allergenic storage protein; FAGAG1; ss.
 XX
 XX Synthetic.
 OS Fagopyrum esculentum.
 XX
 XX WO2003068964-A1.
 XX
 XX 21-AUG-2003.
 PD
 PD 26-SEP-2002; 2002WO-JP009982.
 PF
 PF 15-FEB-2002; 2002JP-00038930.
 PR
 PR (NISS) NISSHIN SEIFUN GROUP INC.
 PA
 PA Yamakawa H, Suzuki E, Miyatake K, Hayakawa K;
 PI

XX
 DR WPI; 2003-637145/60.
 XX
 PT PCR-based method for testing foods using specific primers designed from
 PT genes of target substance, useful in detecting trace components or
 PT identifying specific harmful allergens in (processed) foods.
 PS
 PS Disclosure; Page 10; 38pp; Japanese.
 XX
 CC The present invention describes a method for testing the presence or
 CC absence of a specific substance in a food by performing PCR with primers
 CC which are designed on the basis of data obtained from a part of a gene of
 CC the specific substance. Also described: (1) a similar method for
 CC detecting a trace component contained in a food, or for identifying a
 CC harmful allergen specific to a consumer of such substance by performing a
 CC PCR with primers which are designed on the basis of data obtained from a
 CC part of a gene of the specific substance; (2) primers for PCR applicable
 CC in food testing which are designed on the basis of data obtained from a
 CC part of a gene of the specific substance; and (3) kits for determining
 CC concentration of a specific substance in the food containing the primers.
 CC The methods are useful for testing foods, which can be used in detecting
 CC trace components or identifying specific harmful allergens in (processed)
 CC foods, particularly applicable in food safety and management. The present
 CC sequence represents a PCR primer for a Fagopyrum esculentum major
 CC allergenic storage protein designated FAGAG1, which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 20 BP; 1 A; 11 C; 1 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 55.0%; Score 11; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CTCGCATTCTT 20
 DB 9 CTCGCATTCTT 19
 AC
 AC ADI57250;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE ATP-binding cassette transporter ABCG2 SNP primer #7.
 XX
 XX drug transport capability; polymorphism; ABCG2; polymorphic mutation;
 KW drug sensitivity; anti-cancer drug; cancer therapy;
 KW cancer cell detection; indolocarbazole compound; human;
 KW ABC transporter superfamily;
 KW ATP-binding cassette transporter superfamily;
 KW single nucleotide polymorphism; SNP; PCR; primer; ss.
 XX
 XX Homo sapiens.
 OS
 OS WO2003107249-A1.
 XX
 XX 24-DEC-2003.
 PD
 PD 13-JUN-2003; 2003WO-JP007534.
 PF
 PF 17-JUN-2002; 2002JP-00175806.
 PR
 PR (BANY) BANYU PHARM CO LTD.
 PA
 PA Kotani H, Mizunari S,
 PI
 PI WPI; 2004-156349/15.
 DR
 DR Predicting drug transport capability of mammalian cell by collecting
 PT sample from mammal, determining polymorphism of nucleotide sequence of

PT ABCG2 gene or polymorphism of amino acid sequence of ABCG2 polypeptide.
XX
PS Claim 13; SEQ ID NO 9; 76pp; English.
CC The invention describes a method of predicting a drug transport
CC capability of a mammalian cell involving collecting a sample from a
CC mammal, determining a polymorphism of the nucleotide sequence of ABCG2
CC gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.
CC The method is useful for predicting drug transport capability of a
CC mammalian cell. Polynucleotides comprising single nucleotide
CC polymorphisms or polypeptides comprising polymorphic mutations of the
CC ABCG2 protein are useful as diagnostic agent for diagnosing drug
CC sensitivity which involves analyzing a biological sample from a subject
CC and determining the presence or absence of the polynucleotides or
CC polypeptides, where the subject having the polynucleotides or
CC A transformed cell comprising an ABCG2 protein mutant is useful for
CC measuring drug transport capability. By predicting drug transport
CC capability of a mammalian cell, sensitivity of the indolocarbazole compound,
CC such as anti-cancer drugs can be diagnosed and an indicator for the
CC cancer therapy and, particularly, detecting a cancer cell(s) which is
CC highly sensitive to indolocarbazole compounds, it is now possible to
CC selectively apply the compounds for the therapy. In addition, the optimum
CC dose of the indolocarbazole compounds in the cancer therapy is found and,
CC highly effective method of using the indolocarbazole compounds is
CC provided. This sequence represents a primer used to identify ans sequence
CC single nucleotide polymorphisms of the human ABC transporter superfamily
CC (ATP-binding cassette transporter superfamily) protein ABCG2.
SQ Sequence 20 BP; 11 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 55.0%; Score 11; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 CTCGCATCTT 20
Db 18 CTCGCATCTT 8
RESULT 41
ID ADR96200/c
AD ADR96200 standard; DNA; 20 BP.
XX
AC ADR96200;
XX
DT 06-MAY-2004 (first entry)
XX
DB Primer of the invention #1920.
XX
KW human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS Synthetic.
XX
PN JP2003259875-A.
XX
PD 16-SEP-2003.
XX
PF 08-MAR-2002; 2002JP-00064373.
XX
PR 08-MAR-2002; 2002JP-00064373.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2004-093977/10.
XX
PT Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
PS Claim 2; SEQ ID NO 5229; 2627pp; Japanese.

XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 55.0%; Score 11; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 ATGGCCATCC 13
Db 11 ATGGCCATCC 1
RESULT 42
ID ADN31407
AD ADN31407 standard; DNA; 20 BP.
XX
AC ADN31407;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human forehead box C2 antisense oligonucleotide ISIS227187.
XX
KW Human; ss; antisense; forehead box C2; developmental disorder;
KW lymphedema; lymphedema-distichiasis; dysgenesis; iridocorneal angle;
KW Axenfeld-Rieger anomaly; congenital glaucoma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
XX
PN US2004102621-A1.
XX
PD 27-MAY-2004.
XX
PF 21-NOV-2002; 2002US-00303635.
XX
PR 21-NOV-2002; 2002US-00303635.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KM;
XX
DR WPI; 2004-399740/37.
XX
PT New compound targeted to a nucleic acid molecule encoding forehead box
PT C2, useful in diagnosing and treating developmental disorder.
XX
PS Example 15; SEQ ID NO 72; 80pp; English.
XX
CC The invention relates to a new compound 8-80 nucleobases in length (an
CC antisense oligonucleotide) targeted to a nucleic acid molecule encoding
CC forehead box C2, where the compound specifically hybridises with the
CC nucleic acid molecule encoding human forehead box C2 appearing as
CC ADN3139 and inhibits the expression of forehead box C2. Also included

CC are inhibiting the expression of forkhead box C2 in cells or tissues,
 CC screening for a modulator of forkhead box C2, a diagnostic method for
 CC identifying a disease state, a kit or assay device comprising the
 CC compound and treating an animal having a disease or condition associated
 CC with forkhead box C2. The compound and methods are useful in diagnosing
 CC and treating developmental disorders e.g. lymphedemas such as lymphoedema-
 CC distichiasis, dysgeneses of the mouse Iridocorneal angle similar to those
 CC seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
 CC present sequence is an antisense oligonucleotide targeting forkhead box
 C2.

CC Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCATTC 12
 |||||
 Db 1 CATTGCCATTC 11

RESULT 43

ADN89393
 ID ADN89393 standard; DNA; 20 BP.

XX
 AC ADN89393;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Human CD24 antisense oligonucleotide #72.

XX
 KM ss; human; antisense therapy; CD24; hyperproliferative disorder; probe.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= Other

FT /note= "Phosphorothioate backbone. All cytidines are 5-

FT modified_base 1..5

FT /*tag= a

FT /mod_base= Other

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= Other

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX
 PI Watt AT;

XX
 DR WPI; 2004-389189/36.

XX
 PT New compounds, particularly oligonucleotides targeted to a nucleic acid

XX
 PT encoding CD24, useful for treating diseases associated with CD24, e.g.

XX
 PT hyperproliferative disorders.

XX
 PS Example 15; SEQ ID NO 83; 49pp; English.

XX
 CC The invention relates to antisense oligonucleotides which are targeted

CC to, and inhibit the expression of, nucleic acid encoding human CD24. The

CC antisense oligonucleotides are useful for treating a disease or condition
 CC associated with CD24, such as a hyperproliferative disorder. They are
 CC also useful in research and diagnostics for modulating the expression of
 CC CD24. The present sequence represents a human CD24 antisense
 CC oligonucleotide of the invention.

CC Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCATTC 12
 |||||
 Db 1 CATTGCCATTC 11

RESULT 44

AAQ76368/C
 ID AAQ76368 standard; cDNA; 21 BP.

XX
 AC AAQ76368;

XX
 DT 25-MAR-2003 (revised)

XX
 DT 22-JUN-1995 (first entry)

XX
 DE Oligonucleotide DNA primer 7 to human IGE mRNA.

XX
 KM Epsilon CH4; IGE; immunoglobulin; diagnosis; therapy; hypersensitivity;

XX
 KM oligonucleotide; DNA primer; ss.

XX
 OS Synthetic.

XX
 PN WO9421676-A1.

XX
 PD 29-SEP-1994.

XX
 PF 24-MAR-1994; 94WO-US003243.

XX
 PR 24-MAR-1993; 93US-00037579.

XX
 PA (REGC) UNIV CALIFORNIA.

XX
 PI Saxon A, Zhang K, Max EB;

XX
 DR WPI; 1994-316938/39.

XX
 PT New IGE isoforms and nucleic acid sequences - are used to develop prods.

XX
 PT for diagnosis and treatment of IGE-mediated immune hypersensitivity

XX
 PS conditions.

XX
 PS Disclosure; Page 15; 45pp; English.

XX
 CC This primer was designed to detect human IGE (epsilon) mRNA containing

XX
 CC membrane exon sequences. (Updated on 25-MAR-2003 to correct PN field.)

XX
 CC Sequence 21 BP; 6 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

QY 8 CACTGCCATTC 18
 |||||
 Db 11 CACTGCCATTC 1

RESULT 45

AAA91279/C
 ID AAA91279 standard; DNA; 21 BP.

XX
 AC AAA91279;

XX

DT 06-AUG-2003 (revised)
 DT 08-MAY-2001 (first entry)
 XX
 DE GURAV-5 nucleotide sequence primer LR8-1F.
 XX
 KW GURAV-5; grapevine leafroll virus; GURAV infection; GURAV coat protein;
 KW GURAV HSP70 homologue protein; viral gene mapping; PCR primer;
 XX plant disease resistance; ss.
 OS Grapevine leafroll virus.
 XX
 PN MO200105957-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 19-JUL-2000; 2000WO-US019708.
 XX
 PR 19-JUL-1999; 99US-014453P.
 XX
 PA (AGRI-) AGRITROPE INC.
 XX
 PI Good XC, Monis J;
 XX
 DR WP1; 2001-147339/15.
 XX
 PT Novel grapevine leafroll virus polynucleotide useful as diagnostic and
 PT probe, for viral gene mapping and for induced plant disease resistance.
 XX
 PS Example 3; Page 35; 60pp; English.
 XX
 CC This sequence represents a primer used to isolate the grapevine leafroll
 CC virus (GURAV-5) DNA sequence of the invention. The DNA sequence can be
 CC used in an expression construct. The construct is useful for providing
 CC resistance to GURAV infection in a recombinant plant cell by transforming
 CC the plant cell with it, where transcription of the polynucleotide
 CC sequence interferes with a normal viral function such as movement,
 CC encapsidation or replication of viral RNA. The polynucleotide sequence is
 CC expressed as an antisense sequence and encodes a GURAV coat protein,
 CC preferably a defective GURAV coat protein or a GURAV HSP70 homologue
 CC protein. The GURAV-5 DNA is useful for the synthesis of GURAV, as
 CC diagnostics and probes, for viral gene mapping and for induced plant
 CC disease resistance. It is also useful to detect and quantitate expression
 CC of GURAV in plant tissue prior to use in vegetative propagation, by
 CC detecting the presence of GURAV RNA. (Updated on 06-AUG-2003 to correct
 CC OS field.)
 XX
 SQ Sequence 21 BP; 5 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 55.0%; Score 11; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 ACTCCATTCT 19
 Db 18 ACTCCATTCT 8

Search completed: September 14, 2005, 10:19:43
 Job time : 379 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 09:06:19 / Search time 2413 Seconds
(without alignments)
315.493 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcatgacacatccatctc 20

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 444418

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	70.0	69	8	AZ456041 1M0258U10
C 2	13	65.0	37	8	AZ514485 1M0361F22
C 3	13	65.0	74	9	BX894771 Arabidops
C 4	12	60.0	22	8	AZ828663 2M0105F14
C 5	12	60.0	25	8	AZ658622 1M0535F04
C 6	12	60.0	38	9	TA244G07P
C 7	12	60.0	42	8	AZ818778 T. brucei
C 8	12	60.0	45	8	AZ402282 2M0089E06
C 9	12	60.0	55	1	AA276119 vc36e11.r
C 10	12	60.0	55	5	BP080931 BP080931
C 11	12	60.0	57	8	BZ663993 SALK_0276
C 12	12	60.0	59	6	CB173531 OR_2028E0
C 13	12	60.0	69	8	AZ594221 1M0406K03
C 14	12	60.0	70	1	AA870012 vq10e12.r
C 15	12	60.0	70	4	BG237192 sad04e12.
C 16	12	60.0	73	9	BX919111 Forward s
C 17	12	60.0	74	5	BU949033 vaa04e11.
C 18	12	60.0	76	7	W57143 mds4b04.r1
C 19	12	60.0	78	1	AJ714048 AJ714048
C 20	11	55.0	19	8	AZ418201 1M0194M12
C 21	11	55.0	19	8	AZ822954 2M0096F10
C 22	11	55.0	19	8	AZ967656 2M0238M09
C 23	11	55.0	27	8	AZ427595 1M0209G07
C 24	11	55.0	28	8	AZ615744 1M0445B15

C 25	11	55.0	40	8	AZ417928	AZ417928 1M0193L14
C 26	11	55.0	47	8	AZ769040	AZ769040 1M0569O13
C 27	11	55.0	50	1	AU103440	AU103440 AU103440
C 28	11	55.0	50	1	AU103444	AU103444 AU103444
C 29	11	55.0	50	1	AU103445	AU103445 AU103445
C 30	11	55.0	50	1	AU103448	AU103448 AU103448
C 31	11	55.0	54	7	CN868714	CN868714 001116AAO
C 32	11	55.0	56	6	CB274124	CB274124 ma189a11.
C 33	11	55.0	56	6	AF219060	AF219060 AP219060
C 34	11	55.0	60	8	CC156046	CC156046 NFX123 Ba
C 35	11	55.0	60	9	CR042871	CR042871 Reverse s
C 36	11	55.0	64	6	CB264514	CB264514 54-E02082
C 37	11	55.0	65	8	AZ500380	AZ500380 1M0338O08
C 38	11	55.0	66	9	CR038728	CR038728 Forward s
C 39	11	55.0	68	8	AZ465119	AZ465119 1M0274A22
C 40	11	55.0	69	9	CL888998	CL888998 adf93b07.
C 41	11	55.0	72	7	CN927075	CN927075 000529AEP
C 42	11	55.0	72	8	BH228652	BH228652 106147H0
C 43	11	55.0	72	9	CR055514	CR055514 Forward s
C 44	11	55.0	73	4	BG866118	BG866118 602784943
C 45	11	55.0	74	8	AZ430790	AZ430790 1M0215K19

ALIGNMENTS

RESULT 1
AZ456041/c 69 bp DNA linear GSS 04-OCT-2000
DEFINITION
1M0258U10 Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0258U10 R. genomic survey sequence.

ACCESSION
AZ456041 GI:10614166
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE

1 (bases 1 to 69)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT
Contact: Robert B. Weis
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: J column: 10
Seq primer: CACACGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 69.

FEATURES

SOURCE
1. 69
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0258U10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCACTCCCATCTT 20
Db 62 CCACTCCCATCTT 49

RESULT 2
AZ514485 37 bp DNA linear GSS 05-OCT-2000
LOCUS 1M061F2F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0361F2 F, genomic survey sequence.
ACCESSION AZ514485
VERSION AZ514485.1 GI:10695897
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: F column: 22
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence step: 37.
Location/Qualifiers
1. 37

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361F22"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

ORIGIN

Query Match 65.0%; Score 13; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGCCACTCCCAT 16
Db 34 TTGCCACTCCCAT 22

RESULT 3
BX894771 74 bp DNA linear GSS 05-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-683C03-023158,
DEFINITION genomic survey sequence.
ACCESSION BX894771
VERSION BX894771.1 GI:39927266
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids; eurosid II; Baselliales; Brassicales; Arabidopsids. 1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.

TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K. A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
AUTHORS 4 (bases 1 to 74)
Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.

TITLE Direct Substitution
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g22840. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers

1..74

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-683C03-023158"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 13; DB 9; Length 74;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATCTT 20

Db 41 CACTCCCATCTT 53

RESULT 4

AZ828663/c

LOCUS

22 bp DNA linear GSS 20-FEB-2001

DEFINITION

clone UUGC2M0105114 R, genomic survey sequence.

ACCESSION

AZ828663

VERSION

AZ828663.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiser, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0105

row: 1

column: 14

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0105114"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M.

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 12; DB 8; Length 22;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCATTC 18

Db 13 CCACTCCCATTC 2

RESULT 5

AZ658622

LOCUS

25 bp DNA linear GSS 14-DEC-2000

DEFINITION

clone UUGC1M0535F04 R, genomic survey sequence.

ACCESSION

AZ658622

VERSION

AZ658622.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiser, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0535

row: F

column: 04

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0535F04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCCATCTCTT 20
|||
3 ACTCCCATCTCTT 14

RESULT 6
TA244G07P/c

LOCUS TA244G07P 38 bp DNA linear GSS 13-DEC-2000
DEFINITION T. Brucei sheared genomic DNA clone 244G07, forward sequence,
genomic survey sequence.
ACCESSION AL483538
VERSION AL483538.1 GI:11849039
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS

1 (bases 1 to 38)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, P., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE
JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).

COMMENT

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..38

FEATURES
source

/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927"
/db_xref="taxon:5691"
/clone="244G07"

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATTGCCATCTC 13
|||
21 CATTGCCATCTC 10

RESULT 7
AZ818778/c

LOCUS AZ818778 42 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0089E06F Mouse 10kb plasmid UNGCM library Mus musculus genomic
clone UNGC2M0089E06 F, genomic survey sequence.
ACCESSION AZ818778
VERSION AZ818778.1 GI:12988666
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

REFERENCE
AUTHORS

1 (bases 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
JOURNAL

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0083 row: B column: 06
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 42.

COMMENT

Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0089E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGCM library"
/vector="Vector: pMD22v, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source

1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0089E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGCM library"
/vector="Vector: pMD22v, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches	12; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	7 CCACTCCATTC 18							
Db	13 CCACTCCATTC 2							

RESULT	8
AZ402282/c	
LOCUS	
DEFINITION	
AZ402282	45 bp DNA linear
IM0165G03R Mouse 10kb plasmid UUC1M library Mus musculus genomic	
clone UUC1M0165G03 R, genomic survey sequence.	

ACCESSION	AZ402282	GI:10517356
VERSION	AZ402282..1	
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (pages 1 to 45)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Mouse whole genome scaffolding with paired end reads from 10kbp

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: G column: 03
Seq primer: CACACAGGAACACTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0169G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  

/clone_lib="Mouse 10kb plasmid U06C1M library"  

/notes="Vector: PWD42nv; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA  

was hydrodynamically sheared by repeated passage through a  

0.005 inch orifice at constant velocity. The sheared DNA  

was blunt end-repaired with T4 DNA polymerase and T4  

polynucleotide kinase. Adaptor oligonucleotides were  

ligated to the blunt ends in high molar excess. The  

adaptor DNA was purified and size-selected for a 9.5 to  

10.5 kb range using preparative agarose gel  

electrophoresis. Vector DNA was prepared from a derivative  

of PWD42 (g14732114[gB]/Af129072.1)', a copy-number  

inducible derivative of plasmid RI. The vector was ligated  

with adaptors complementary to the insert adaptors and  

purified. The sheared, adaptor DNA was annealed to  

adaptor vector DNA, and transformed into  

chemically-competent E. coli XL10-Gold (Stratagene) cells  

and selected for ampicillin resistance."

```

Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	7	CCACTCCCATTC	18						
Db	35	CCACTCCCATTC	24						

RESULT 9	LOCUS	DEFINITION	CHAIN 4 ;
AA276119	AA276119	55 bp mRNA linear EST 01-APR-1997	
	v336e11.1	Baretead MPEIRB1 Mus musculus cDNA clone IMAGE:776684 5'	
		similar to SW:NTM MOUSE P03911 NADH-UBIQUINONE OXIDOREDUCTASE	
		mRNA sequence.	

ACCESSION	AA276119	GI:1918749
VERSION	AA276119.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

ORGANISM
Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Mus.
1 (bases 1 to 55)
REFERENCE
AUTHORS
Marral, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gatta, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project

WashU-HM1 Mouse BSI Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:469540
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2. ET from Amersham
High quality sequence stop: 1.

```

source
1.:53
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:776684"
/sex="mixed"
/tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DHL0B"
/clone_id="Barstead MPRB1"
/notes="Vector: pRTT3-Pac (Pharmacia) with a modified
polymer; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTGGGAGCGGCGGCTTTTTTTTTTTTTTTTTT
3']; double stranded cDNA was ligated to Eco RI adaptors
[CAAGATCTGGAC], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pRTT3 vector.
Library constructed by Bob Barstead."

```

ORIGIN	Query Match	60.0%	Score 12;	DB 1;	Length 55;
	Best Local Similarity	100.0%	Pred. No. 1.5e+04;		
Matches	12;	Conservative	0;	Mismatches	0;
				Indels	0;
QY	8 CACTGCCATTCT	19			
DB	21 CACTGCCATTCT	32			

```

RESULT 10
BP080931/c
LOCUS      BP080931      55 bp      mRNA      linear      EST 27-AUG-2004
DEFINITION BP080931 Lotus japonicus roots Lotus corniculatus var. japonicus
            cDNA clone MR064f09_f_3', mRNA sequence.
ACCESSION  BP080931
VERSION     BP080931.1
KEYWORDS   GI:45637592
SOURCE     EST.
ORGANISM   Lotus corniculatus var. japonicus (Lotus japonicus)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
            Lotus.
            1 (bases 1 to 55)
REFERENCE  Asamizu,F., Nakamura,Y., Sato,S. and Tabata,S.
AUTHORS   Characteristics of the Lotus japonicus Gene Repertoire Deduced from
TITLE      Large-Scale Expressed Sequence Tag (EST) Analysis
JOURNAL    Plant Mol. Biol. 54 (3), 405-414 (2004)
COMMENT    Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kasarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
            Location/Qualifiers
            1..55
            /organism="Lotus corniculatus var. japonicus"
            /mol_type="mRNA"
            /isolate="Miyakojima MG-20"
            /db_xref="taxon:34305"
            /clone="MR064f09_f_3"
            /issue_type="Roots"
            /clone_1lb="Lotus japonicus roots"

ORIGIN
Query Match      60.0%; Score 12; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTGCCACTCCCA 15
Db      43 TTGCCACTCCCA 32

RESULT 11
B2663993
LOCUS      B2663993      57 bp      DNA      linear      GSS 31-JAN-2003
DEFINITION B2663993.43.05.x Arabidopsis thaliana TDNA insertion line
            Arabidopsis thaliana genomic clone SALK_027603.43.05.x, genomic
            survey sequence.
ACCESSION  B2663993
VERSION     B2663993.1
KEYWORDS   GI:28180086
SOURCE     GSS.
ORGANISM   Arabidopsis thaliana (thale cress)
            Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 57)
REFERENCE  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
AUTHORS   Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shim,P., Zimmerman,U. and Ecker,J.R.
TITLE      A Sequence-indexed Library of Insertion Mutations in the
JOURNAL    Arabidopsis Genome
COMMENT    Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of

```

```

            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
            1..57
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone="SALK_027603.43.05.x"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocol used can
            be found at http://signal.salk.edu/tDNA_protocol.html"

ORIGIN
Query Match      60.0%; Score 12; DB 8; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATTGCCACTCCC 14
Db      18 ATTGCCACTCCC 29

RESULT 12
CB173531/c
LOCUS      CB173531      59 bp      mRNA      linear      EST 09-OCT-2003
DEFINITION CB173531 OR_2028E03_010501.y1 Adult mouse olfactory epithelium library Mus
            musculus cDNA clone 2028E03 5', mRNA sequence.
ACCESSION  CB173531
VERSION     CB173531.1
KEYWORDS   GI:37592160
SOURCE     EST.
ORGANISM   Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 59)
REFERENCE  Young,J.M., Shykind,B.M., Lane,R.P., Tomes-Priddy,L., Ross,J.A.,
AUTHORS   Walker,M., Williams,E.M. and Trask,B.J.
TITLE      Odorant receptor expressed sequence tags demonstrate olfactory
            expression of over 400 genes, extensive alternate splicing and
            unequal expression levels
JOURNAL    Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT    Contact: Young JM
            Trask Lab, Division of Human Biology
            Fred Hutchinson Cancer Research Center
            1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
            98109-1024 USA
            Tel: 206 667 1471
            Fax: 206 667 6524
            Email: jayoung@fhcrc.org
            Seq primer: M13 Reverse.
            Location/Qualifiers
            1..59
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="2028E03"
            /issue_type="Olfactory and respiratory epithelium"
            /dev_stage="Adult"
            /note="Organ: Olfactory epithelium library"
            lambdaZAPII-XR, Site 1: EcoRI; Site 2: XhoI. This library
            was provided by Leslie Voshell. mRNA was prepared from
            the olfactory and respiratory epithelium of an adult
            mouse. Oligo-dT primed cDNA was directionally cloned into
            Stratagene's lambdaZAPII-XR vector."

ORIGIN
Query Match      60.0%; Score 12; DB 6; Length 59;

```


RESULT 15
BG237192

LOCUS BG237192 70 bp mRNA linear EST 23-JUL-2004
 DEFINITION bab04912.y1 Gm-c1071 glycine max cdna clone genome systems clone
 ID: Gm-c1071-719 5', mRNA sequence.
 BG237192
 ACCESSION BG237192
 VERSION BG237192.1 GI:12772265
 KEYWORDS EST.

SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosoid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine

REFERENCE 1 (bases 1 to 70)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V.,
 Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
 Beck,C., Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M.,
 Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N.,
 Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterson,R. and Wilson,R.
 PUBLIC SOYBEAN EST PROJECT
 UNPUBLISHED (1999)
 CONTACT: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: es@watson.wustl.edu

TITLE JOURNAL
 COMMENT

FEATURES
 source
 1..70
 location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1071-719"
 /issue_type="immature pods (-2cm long) of greenhouse grown plants"
 /lab_host="DH10B"
 /clone_id="Gm-c1071"
 /note="Vector: pSPORT1, Site 1: NotI; Site 2: SalI; The cDNA library was constructed from mRNA isolated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. email: l-vodkin@uiuc.edu"

ORIGIN

Query Match 60.0%; Score 12; DB 4; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGCACCTCCCAT 16
 |||||||||
 DB 19 TGCACCTCCCAT 30

RESULT 16
BX91911/c

LOCUS BX91911/c 73 bp DNA linear GSS 05-JUL-2004
 DEFINITION Forward strand read from insert in 3'HPT insertion targeting and
 chromosome engineering clone MHP384e03, genomic survey sequence.
 BX91911
 ACCESSION BX91911.1 GI:49723369
 VERSION BX91911.1
 KEYWORDS GSS; genome survey sequence; MICEP.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 73)
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 DIRECT SUBMISSION
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICEP

TITLE JOURNAL
 COMMENT

FEATURES
 source
 1..73
 location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHP384e03"
 /clone_id="MHP"

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGCACCTCCCAT 16
 |||||||||
 DB 21 TGCACCTCCCAT 10

RESULT 17
 BU9494033/c 74 bp mRNA linear EST 01-OCT-2002
 LOCUS BU9494033
 DEFINITION va04e11.y2 SV DOGRDA RD3 Canis familiaris CDNA 5', mRNA sequence.
 ACCESSION BU9494033
 VERSION BU9494033.1 GI:22790291
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 74)
 AUTHORS Virgin,S., Tianxiang,S., Karst,S., Wobus,C., Lay,M., Clifton,S.,
 Page,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M.,
 Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J.,
 Ronko,I., Tsagarashvili,R., Maguire,L., Kennedy,S., Waterson,R.

TITLE RNA Expression in Diseased Tissues by RNA
 JOURNAL UNPUBLISHED (2002)
 COMMENT Other ESTs: va04e11.x2
 CONTACT: Skip Virgin
 RNA Expression in Diseased Tissues by RDA
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: es@watson.wustl.edu

Library was constructed by Tianxiang Shen and Skip Virgin DNA
 sequencing by: Washington University Genome Sequencing Center for
 information on obtaining a clone please contact: Skip Virgin
 (virgin@immunology.wustl.edu)
 Seq primer: -40RP from Gidco.
 Location/Qualifiers
 1..74
 /organism="Canis familiaris"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9615"
/tissue_type="Brain from a dog with encephalitis"
/lab_host="DH5a"
/clone_1lb="SV DGRDA RD3"
/note="Vector: PCR2.1-TOPO, PCR products were directly cloned into TA cloning vector (pre-cut vector PCR2.1-TOPO was purchased from Invitrogen) Average insert size is 300bp. Our insert also have same adaptor sequence on both ends. The sequence of the adaptor is:
5'-ATACGTACAGCTGCTTACATCTG-3'."

Query Match 60.0%; Score 12; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCATCTC 13
|||||
17 CATTGCCATCTC 6

RESULT 18 76 bp mRNA linear EST 04-JUN-1996
W57143/c clone IMAGE:372175 5' similar to PIR:S54157 S54157 extensin-1like protein - cowpea, mRNA sequence.

ACCESSION W57143.1 GI:1359002
VERSION W57143.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 76)

AUTHORS Marra,M., Haller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheinberg,K., Stepec,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watsn.wustl.edu

FEATURES This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:233607
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: ETPRimer
High quality sequence stop: 1.
Location/Qualifiers

1..76
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:372175"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_1lb="Soares mouse embryo NBMEL3.5 14.5"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I, Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT

ORIGIN

T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 1]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Benito Soares and M.Fatima Bonaldo."

Query Match 60.0%; Score 12; DB 7; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATCTT 19
|||||
76 CACTCCCATCTT 65

RESULT 19 78 bp mRNA linear EST 30-JUN-2004
AJ714048 LKPD01 Homo sapiens cDNA clone LKPD02463, mRNA sequence.
AJ714048/c
LOCUS AJ714048
DEFINITION AJ714048
ACCESSION AJ714048
VERSION AJ714048.1 GI:49499660
KEYWORDS EST.
SOURCE Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 78)

REFERENCE Depitta,C., Tomboian,L., Kronmle,G., Romualdi,C., Vitulo,N., Basso,G. and Lanfranchi,G.
A leukemia-enriched cDNA microarray platform identified new transcripts with relevance to the biology of leukemias

JOURNAL Unpublished (2004)
COMMENT Contact: Depitta C
Biology and CRIBI
University of Padova
Via U. Bassi, 58/B, 35131, ITALY.

FEATURES Location/Qualifiers
1..78
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LKPD02463"
/tissue_type="bone marrow"
/clone_1lb="LKPD01"
/note="Caucasian"

ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCAT 16
|||||
Db 61 TGGCACTCCCAT 50

RESULT 20 19 bp DNA linear GSS 03-OCT-2000
AZ418201 1M0194M12F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0194M12 F, genomic survey sequence.
LOCUS AZ418201
DEFINITION AZ418201
ACCESSION AZ418201.1 GI:10542214
VERSION AZ418201.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellam,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0194 row: M column: 12
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0194M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 CTCGCATTCTT 20
|||||
Db 7 CTCGCATTCTT 17
|||||

RESULT 21
AZ822954/c 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0036110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0096110 R, genomic survey sequence.
ACCESSION AZ822954
VERSION AZ822954.1 GI:12992862
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellam,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: I column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096110"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 CCACTCCATT 17
|||||
Db 15 CCACTCCATT 5
|||||

RESULT 22
AZ967656/c 19 bp DNA linear GSS 27-APR-2001
LOCUS 2M0238M09R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0238M09 R, genomic survey sequence.
ACCESSION AZ967656
VERSION AZ967656.1 GI:13838883
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0238 row: M column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0238M09"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number:
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
7 CCACTCCCAT 17
|||
Db 16 CCACTCCCAT 6

RESULT 23
AZ427595/c 27 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION
IM0209G07R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0209G07 R, genomic survey sequence.
ACCESSION
AZ427595
VERSION
AZ427595.1 GI:10551608
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 27)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0209 row: G column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0209G07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number:
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
7 CCACTCCCAT 17
|||
Db 17 CCACTCCCAT 7

RESULT 24
AZ615744/c 28 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
IM0445B15F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0445B15 F, genomic survey sequence.
ACCESSION
AZ615744
VERSION
AZ615744.1 GI:11737934
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 28)

AUTHORS

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Baecron, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud M. Meemeh, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niedelhausen, A. and Wright, D., Weiss, K.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss

TITLE

AUTHORS

TITLE

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmood, M., Meinen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokoe, R., Tinney, A., von
Miedendorfs, A. and Wright, D., Weiser, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiser

JOURNAL
COMMENT

FEATURES

Bourse

1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TUGC1M0445B15"
/sex="Male"
/lab_host="5. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid TUGC1M library"
/note="Vector: PM242nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PM242 (g11473114[gb]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```
Query Match          55.0%; Score 11; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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QY	7	CCACTCCCATTT	17
Db	26	CCACTCCCATTT	16

RESULT 25
AZ417928/

LOCUS	AZ417928	40 bp	DNA	linear	SSS 03-OCT-2000				
DEFINITION	IM019313L14R Mouse 10kb plasmid UGSCM library Mus musculus genomic clone UGSCM019314 R, genomic survey sequence.								
ACCESSION	AZ417928								
VERSION	AZ417928.1								
KEYWORDS	SSS. GI:10541941								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								

REFERENCE

1 (bases 1 to 40)

FEATURES

Source

1. 40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0193L14"
/sex="Male"
/lab_host="E. coli strain XL10-Gold T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid UUCG1M library"
/note="Vector: pMD22ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrothermally sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g14732114[gb/AP129072.1]), a copy-number
inductible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```
Query Match      55.0%; Score 11; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 11; Conservative 0. Mismatches 111
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QY	7	CGACTCCGATT	17
Db	24	CGACTCCGATT	14

RESULT 26

AZ769040	AZ769040	47 bp	DNA	linear	GSS 16-FEB-2001
LOCUS					
DEFINITION	1M0569013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic				
ACCESSION	clone UUGC1M0569013 F, genomic survey sequence.				
VERSION	AZ769040				
KEYWORDS	AZ769040.1 GI:12888765				
SOURCE	GSS.				
ORGANISM	Mus musculus (house mouse)				
	Mus musculus				

REFERENCE

1 (bases 1 to 47) ... Muridae; Mus.

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)

JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Sd Error: 0.00
Plate: 0569 row: 0 column: 13
Seq primer: CGTTGTAAACGACGCGCCACT
Class: Plasmid ends
High quality sequence stop: 47.
Location/Qualifiers

FEATURES
source
1..47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0569013"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1[4732114]gb[AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
9 ACTCCCATCT 19
|||||
21 ACTCCCATCT 31

Db
21 ACTCCCATCT 31

RESULT 27
AUI03440 50 bp mRNA linear EST 28-JAN-2004
AUI03440
LOCUS
DEFINITION
AUI03440 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP01378, mRNA sequence.
ACCESSION
AUI03440
VERSION
AUI03440.1 GI:13552961
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 50)

AUTHORS
Suzuki, Y., Tajira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Kata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
MEDLINE
11375929
PUBMED
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP01378"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4 TTGCCACTCCC 14
|||||
26 TTGCCACTCCC 36

Db
26 TTGCCACTCCC 36

RESULT 28
AUI03444 50 bp mRNA linear EST 28-JAN-2004
AUI03444
LOCUS
DEFINITION
AUI03444 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP03841, mRNA sequence.
ACCESSION
AUI03444
VERSION
AUI03444.1 GI:13552965
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 50)
Suzuki, Y., Tajira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Kata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
MEDLINE
11375929
PUBMED
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCC 14
|||||
31 TTGGCACTCCC 41

Db 31 TTGGCACTCCC 41

RESULT 29
AUI03445 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03842, mRNA sequence.
ACCESSION AUI03445 GI:13552966
VERSION AUI03445.1 GI:13552966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

TITLE Location/Qualifiers
JOURNAL 1. 50
MEDLINE /organism="Homo sapiens"
PUBMED /mol_type="mRNA"
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03842"

ORIGIN
Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCC 14
|||||
26 TTGGCACTCCC 36

Db 26 TTGGCACTCCC 36

RESULT 30
AUI03448 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03448 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP05740, mRNA sequence.
ACCESSION AUI03448 GI:13552969
VERSION AUI03448.1 GI:13552969
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP05740"

ORIGIN
Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCC 14
|||||
39 TTGGCACTCCC 49

Db 39 TTGGCACTCCC 49

RESULT 31
CN868714 54 bp mRNA linear EST 03-JUN-2004
LOCUS CN868714
DEFINITION 00116AAOA002279RT (AAOA) Royal Gala phloem Malus x domestica cDNA
clone AAOA002279, mRNA sequence.
ACCESSION CN868714
VERSION CN868714.1 GI:48126250
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 54)
Beuning,L., Bowen,D., Crowhurst,R., Glaeve,A., Jansen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Glaeve,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES
source
1. 54
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAOA002279"
/rname_type="Phloem, scrapings from inside of bark mature
wood"
/clone_1b=" (AAOA) Royal Gala phloem"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

ORIGIN
Query Match 55.0%; Score 11; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;

Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCC 14
|||||
31 TTGGCACTCCC 41

Db 31 TTGGCACTCCC 41

RESULT 29
AUI03445 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03842, mRNA sequence.
ACCESSION AUI03445 GI:13552966
VERSION AUI03445.1 GI:13552966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

TITLE Location/Qualifiers
JOURNAL 1. 50
MEDLINE /organism="Homo sapiens"
PUBMED /mol_type="mRNA"
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP05740"

ORIGIN
Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCC 14
|||||
26 TTGGCACTCCC 36

Db 26 TTGGCACTCCC 36

RESULT 30
AUI03448 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03448 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP05740, mRNA sequence.
ACCESSION AUI03448 GI:13552969
VERSION AUI03448.1 GI:13552969
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP05740"

ORIGIN
Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCC 14
|||||
39 TTGGCACTCCC 49

Db 39 TTGGCACTCCC 49

RESULT 31
CN868714 54 bp mRNA linear EST 03-JUN-2004
LOCUS CN868714
DEFINITION 00116AAOA002279RT (AAOA) Royal Gala phloem Malus x domestica cDNA
clone AAOA002279, mRNA sequence.
ACCESSION CN868714
VERSION CN868714.1 GI:48126250
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 54)
Beuning,L., Bowen,D., Crowhurst,R., Glaeve,A., Jansen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Glaeve,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES
source
1. 54
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAOA002279"
/rname_type="Phloem, scrapings from inside of bark mature
wood"
/clone_1b=" (AAOA) Royal Gala phloem"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

ORIGIN
Query Match 55.0%; Score 11; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TGGCACTCCCA 15
|||||
Db 19 TGGCACTCCCA 29

RESULT 32
CB274124 56 bp mRNA linear EST 24-FEB-2003
CB274124
IMAGE:6448532 5', mRNA sequence.
DEFINITION
CB274124.1 GI:28464447
ACCESSION
CB274124.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 56)
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
Martin, J., Wylie, T., Danne, M., Bowers, Y., Theising, B., Gibbons, M.,
Ritter, E., Tsagaris, H., R., Ronko, I., Maguire, L., Kennedy, S.,
Benmet, J., Watson, R. and Wilson, R.
NIEHS Mouse
Unpublished (2002)
Contact: McCarrey/Eddy NIEHS Mouse

TITLE
JOURNAL
COMMENT
NIEHS Mouse
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: east@watson.wustl.edu
Library constructed and donated by J. McCarrey, Ph.D. (Southwest
Foundation for Biomedical Research, Dept. of Genetics) - excision
done by E.M. Eddy, Ph.D. (National Institutes of Health, National
Institute of Environmental Health Sciences).
MGI:2072492
Seq primer: Primer name ambiguous
High quality sequence stop: 52.
Location/Qualifiers

1. .56
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:6448532"
/sex="male"
/tissue_type="round spermatids, pooled from multiple mice"
/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/note="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site_1: XhoI; Site_2: EcoRI; cDNA oligo
dt-primed [5'-(GA)10-ACTAGTCTCAGTCTTTTCTT-3'] and
directionally cloned using 5' linkers 5'-AATCGCGCAG-3'
and 5'-CTCGTCCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-unifap-XR) and resulting
single-stranded phagemids were prepiped and transformed
into DH10B. Library contains 98.5% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63423."

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACT 11
|||||
Db 38 GCATTGCCACT 48

RESULT 33
AF219060/c 56 bp DNA linear GSS 17-APR-2000
AF219060
DEFINITION
AF219060 Human Homo sapiens genomic clone Gf9, genomic survey
sequence.
ACCESSION
AF219060
AF219060.1 GI:7581506
VERSION
AF219060.1
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 56)
Hanshure, M., Cross, S., Daniels, M., Lennon, G. and Brook, J.D.
A transcript map of a 10-Mb region of chromosome 19: A source of
genes for human disorders, including candidates for genes involved
in asthma, heart defects, and eye disorders
Genomics 63 (3), 425-429 (2000)
JOURNAL
MEDLINE
20171383
10704290
Contact: Hanshure M
Institute of Genetics
University of Nottingham
Queen's Medical Center, Nottingham, NG7 2UL, United Kingdom
Class: exon-trapped.
Location/Qualifiers

FEATURES
source
1. .56
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Gf9"
/clone_lib="Human"

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 CTCGCATTCTT 20
|||||
Db 52 CTCGCATTCTT 42

RESULT 34
CC156046/c 60 bp mRNA linear GSS 01-APR-2004
CC156046
DEFINITION
NFX123 BayGenomics Gene Trap Library pGTLdelta;Tmpts Mus musculus
cDNA, mRNA sequence.
ACCESSION
CC156046
CC156046.2 GI:46014502
VERSION
CC156046.2
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 60)
BayGenomics.
TITLE
http://baygenomics.ucsf.edu/
JOURNAL
Unpublished (2001)
COMMENT
On Apr 1, 2004 this sequence version replaced gi:30109402.
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?
 OPTION=EXACT&TYPE=CELL_LINE&KEY=NPX123
 Class: Gene Trap.

FEATURES
 SOURCE
 Location/Qualifiers
 1..60

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Ola"
 /db_xref="taxon:10090"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /clone_lib="BayGenomics Gene Trap Library
 pGRTdelta.TMps"
 /note="Vector: pGRTdelta.TMps"

Query Match
 Best Local Similarity 55.0%; Score 11; DB 8; Length 60;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
 |||||
 Db 22 TGGCACTCCCA 12

RESULT 35
 LOCUS CR042871/c 60 bp DNA linear GSS 05-JUL-2004
 DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
 ACCESSION CR042871
 VERSION chromosome engineering clone MHP272c17, genomic survey sequence.
 KEYWORDS GSS, genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 60) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Rogers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Jones,J., and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES
 SOURCE
 Location/Qualifiers
 1..60

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHP272c17"
 /clone_lib="MHP"

Query Match
 Best Local Similarity 55.0%; Score 11; DB 9; Length 60;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
 |||||
 Db 30 TGGCACTCCCA 20

RESULT 36
 LOCUS CB264514 64 bp mRNA linear EST 06-NOV-2003
 DEFINITION 54-B020827-035-004-P01q-T7R MP1Z-ADIS-035 Arabidopsis thaliana cDNA
 ACCESSION CB264514
 VERSION clone MP1Z2000P014Q 5-PRIME, mRNA sequence.
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 64)

REFERENCE
 AUTHORS Schmidt,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
 Mitchell-Olds,T. and Weishaar,B.
 TITLE Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
 MEDLINE 22683290
 PUBMED 12799357

COMMENT
 Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert length: 64 Std Error: 0.00
 Plate: 4 Row: 1 column: 01
 Seq primer: T7R; CTATACGACTCACTATAGGA.
 Location/Qualifiers
 1..64

FEATURES
 SOURCE

/organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /cultiivar="Achkarren-2 (Ak-2)"
 /db_xref="GBI:594855"
 /db_xref="taxon:3702"
 /clone="MP1Z2000P014Q"
 /tissue="inflorescence"
 /lab_host="E. coli TOP10"
 /clone_lib="MP1Z-ADIS-035"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; cDNA
 library from Arabidopsis thaliana, accession Achkarren-2;
 inflorescences from flower buds to young siliques; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites SalI-NotI,
 T7-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-SPE; Note:
 Sequencing granted in the context of the GABI Arabidopsis
 Verbund1: Genetic diversity, 'Establishment of
 high-efficiency SNP-based mapping tools and development of
 methods for genome-wide mutation detection' PI Bernd
 Weishaar; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de This clone
 is available from RZPD; contact RZPD (clone@rzpd.de) for
 further information."

ORIGIN

Query Match
 Best Local Similarity 55.0%; Score 11; DB 6; Length 64;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCCCACTCTT 20
 |||||
 Db 34 CTCCCACTCTT 44

RESULT 37
 LOCUS AZ500380/c 65 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0338008R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ACCESSION AZ500380
 VERSION clone UUGC1M0338008 R, genomic survey sequence.
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 65) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tilney,A., von
 Niederhausern,A. and Wright,D., Weisb,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL Plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 033 row: 0 column: 08
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 65.

FEATURES
 source

1. .65
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UIGC1M0338008"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UIGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 65;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACCTCCCAT 17
 |||||
 Db 58 CCACCTCCCAT 48

RESULT 38
 CRO38728/c 66 bp DNA linear GSS 05-JUL-2004
 LOCUS Forward strand read from insert in 3'HPRT insertion targeting and
 DEFINITION chromosome engineering clone MHP115n17, genomic survey sequence.
 CRO38728
 ACCESSION CRO38728.1 GI:49771783
 VERSION GSS; genome survey sequence; MICEP.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 66)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICEP

FEATURES
 source

1. .66
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHP115n17"
 /clone_1lb="MHP115n17"

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 66;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGCACCTCCCA 15
 |||||
 Db 33 TGCACCTCCCA 23

RESULT 39 68 bp DNA linear GSS 04-OCT-2000
 AZ465119/c
 LOCUS 1M0274A22R Mouse 10kb plasmid UIGC1M library Mus musculus genomic
 DEFINITION clone UIGC1M0274A22 R, genomic survey sequence.
 AZ465119
 ACCESSION AZ465119.1 GI:10623244
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus

REFERENCE

1 (bases 1 to 68)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D. Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0274 row: A column: 22
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 68.

FEATURES

source

1. .68
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UIGC1M0274A22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UIGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 68;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACCTCCCATTT 17
|||||
Db 67 CCACCTCCCATTT 57

RESULT 40
CL888998 69 bp DNA linear GSS 30-AUG-2004
LOCUS abe93b07.x1 soybean random, unfiltered genomic library Glycine max
DEFINITION CL888998
ACCESSION CL888998
VERSION CL888998.1 GI:51632383
KEYWORDS GSS.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 69)
Numbering: A., Bedell, J.A., Citek, R.W., Robbins, D., McNamey, J., Peterson, S., Jones, J., Files, J., Budiman, M.A., Nguyen, H. and Stacey, G.
Methylation filtered genomic sequences from Glycine max unpublished (2004)
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LidID: 230
Class: Shotgun.

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT

Location/Qualifiers
1. .69
/organism="Glycine max"
/mol_type="genomic DNA"
/cultiyar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="soybean random, unfiltered genomic library"
/note="Vector: POT2; Site_1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut POT2. LidID: 230"

FEATURES

source

1. .69
/organism="Glycine max"
/mol_type="genomic DNA"
/cultiyar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="soybean random, unfiltered genomic library"
/note="Vector: POT2; Site_1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut POT2. LidID: 230"

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCCTCATTTCTT 20
|||||
Db 48 CTCCTCATTTCTT 58

RESULT 41
CN927075

LOCUS CN927075 72 bp mRNA linear EST 07-JUN-2004
DEFINITION 000529ABEA002800HT (ABPA) Pinkie expanding leaf Malus x domestica
ACCESSION CN927075
VERSION CN927075.1 GI:48399888
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 72)
Beunty, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT

Location/Qualifiers
1. .72
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="ABPA002800"
/tissue_type="Leaf"
/dev_stage="Expanding"
/clone_lib="(ABPA) Pinkie expanding leaf"
/note="Vector: pBR-CMV; Library sequenced by Genesis Research & Development"

ORIGIN

Query Match 55.0%; Score 11; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCCC 14
|||||
Db 54 TTGCCACTCCC 64

RESULT 42
BH228652 72 bp DNA linear GSS 08-NOV-2001
LOCUS 1006147H09.2BL x1 1006 - Rescenu Grid G Zea mays genomic, genomic
DEFINITION BH228652
ACCESSION BH228652
VERSION BH228652.1 GI:16829902
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 72)
Walbot, V.
Maize genomic sequences found using engineered Rescenu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006147 row: 8
Class: transposon-tagged.

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES

SOURCE

Location/Qualifiers

1..72

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/issue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_1lb="1006 - RescueMu Grid G"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcribed units. For more information on RescueMu, go to the web site 'www.zmldb.iastate.edu' and follow the links for 'RescueMu'; Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match

55.0%; Score 11; DB 8; Length 72;

Best Local Similarity 100.0%; Pred. No. 6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

6 GCCACTCCCAT 16

Db

6 GCCACTCCCAT 16

RESULT 43

LOCUS

CR055514 72 bp DNA linear GSS 05-JUL-2004

DEFINITION Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP136108, genomic survey sequence.

ACCESSION

CR055514

VERSION

CR055514.1

KEYWORDS

GSS; genome survey sequence; MICR.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 72)

AUTHORS

Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.

TITLE

Direct Submision

JOURNAL

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA UK. <http://www.sanger.ac.uk/MICR>

FEATURES

Location/Qualifiers

SOURCE

1..72

ORGANISM

/organism="Mus musculus"

VERSION

/mol_type="genomic DNA"

KEYWORDS

/db_xref="taxon:10090"

SOURCE

/clone="MHP136108"

ORGANISM

/clone_1lb="MHP"

ORIGIN

Query Match

55.0%; Score 11; DB 9; Length 72;

Best Local Similarity 100.0%; Pred. No. 6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GCATTGCCACT 11

Db

42 GCATTGCCACT 52

RESULT 44

LOCUS

BG866118

73 bp

mRNA

linear

EST 29-MAY-2001

DEFINITION

602784943F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910987 5', mRNA sequence.

ACCESSION

BG866118

VERSION

BG866118.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 73)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

plate: LLAM10812

High quality sequence stop: 73.

FEATURES

Location/Qualifiers

1..73

SOURCE

/organism="Mus musculus"

mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4910987"

/lab_host="DH10B (T1 phage-resistant)"

/clone_1lb="NCI_CGAP_SG2"

/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match

55.0%; Score 11; DB 4; Length 73;

Best Local Similarity 100.0%; Pred. No. 6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 CATTGCCACTC 12

Db

42 CATTGCCACTC 52

RESULT 45

LOCUS

A2430790/c

DEFINITION

1M0215K19F Mouse 10kb plasmid UGCM1 library Mus musculus genomic clone UGCM0215K19 F, genomic survey sequence.

ACCESSION

A2430790

VERSION

A2430790.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 74)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah

Genome Center

Bldg. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0215 row: K column: 19
 Seq primer: GGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 74.
 Location/Qualifiers
 1..74

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC1M021SK19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UNGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 74;
 Best Local Similarity 100.0%; Freq. No. 6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 CCACTCCCATTT 17
 Db 59 CCACTCCCATTT 49

Search completed: September 14, 2005, 11:43:51
 Job time : 2421 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 09:46:31 ; Search time 122 Seconds
(without alignments)
268.242 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20
Sequence: 1 gcatgccaccatccatctt 20

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1296172

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

Database : Issued_Patents_MA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	65.0	54	US-08-956-171E-2606	Sequence 2606, App
C 2	13	65.0	54	US-08-781-986A-2606	Sequence 2606, App
C 3	12	60.0	21	US-09-262-773-113	Sequence 113, App
C 4	12	60.0	25	US-09-396-196G-64405	Sequence 64405, A
C 5	12	60.0	25	US-09-396-196G-106332	Sequence 106332, A
C 6	12	60.0	25	US-09-396-196G-106333	Sequence 106333, A
C 7	12	60.0	25	US-09-396-196G-106334	Sequence 106334, A
C 8	12	60.0	29	US-08-846-012A-8	Sequence 8, Appli
C 9	12	60.0	29	US-09-100-297-8	Sequence 8, Appli
C 10	12	60.0	39	US-09-052-995-8	Sequence 8, Appli
C 11	11	55.0	17	US-08-758-306-997	Sequence 997, App
C 12	11	55.0	18	US-09-690-185A-5	Sequence 5, Appli
C 13	11	55.0	18	US-08-853-14C-5	Sequence 46, Appli
C 14	11	55.0	19	US-09-230-186-46	Sequence 5, Appli
C 15	11	55.0	20	US-09-403-861A-4	Sequence 4, Appli
C 16	11	55.0	25	US-09-396-196G-26004	Sequence 26004, A
C 17	11	55.0	25	US-09-396-196G-26005	Sequence 26005, A
C 18	11	55.0	25	US-09-396-196G-72679	Sequence 72679, A
C 19	11	55.0	25	US-09-396-196G-91273	Sequence 91273, A
C 20	11	55.0	25	US-09-396-196G-91273	Sequence 91273, A
C 21	11	55.0	42	US-07-834-539A-24	Sequence 24, Appli
C 22	11	55.0	42	US-08-053-131-32	Sequence 32, Appli
C 23	11	55.0	42	US-08-645-641-32	Sequence 32, Appli
C 24	11	55.0	42	US-07-853-408B-32	Sequence 32, Appli
C 25	11	55.0	42	US-08-096-762-32	Sequence 24, Appli
C 26	11	55.0	42	US-08-800-353-24	Sequence 24, Appli
C 27	11	55.0	42	US-08-308-865-32	Sequence 32, Appli

C 28	11	55.0	42	US-09-042-353-200	Sequence 200, App
C 29	11	55.0	42	US-08-758-417A-48	Sequence 48, Appli
C 30	11	55.0	42	PCT-US92-06185-24	Sequence 24, Appli
C 31	11	55.0	42	PCT-US92-10983-32	Sequence 32, Appli
C 32	10	50.0	12	US-08-441-887A-59	Sequence 59, Appli
C 33	10	50.0	15	US-09-081-646-147	Sequence 147, App
C 34	10	50.0	15	US-09-081-646-830	Sequence 830, App
C 35	10	50.0	18	US-09-213-719-54	Sequence 54, Appli
C 36	10	50.0	18	US-09-422-978-8213	Sequence 8213, Ap
C 37	10	50.0	18	US-09-155-885A-267	Sequence 267, App
C 38	10	50.0	19	US-09-422-978-5302	Sequence 5302, Ap
C 39	10	50.0	19	US-09-696-791-3881	Sequence 3881, Ap
C 40	10	50.0	19	US-09-696-791-3882	Sequence 3882, Ap
C 41	10	50.0	20	US-10-141-021-15	Sequence 15, Appli
C 42	10	50.0	20	US-10-141-103-15	Sequence 15, Appli
C 43	10	50.0	20	US-10-141-063-15	Sequence 15, Appli
C 44	10	50.0	20	US-10-141-094-15	Sequence 15, Appli
C 45	10	50.0	20	US-10-141-060-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-956-171E-2606/c
Sequence 2606, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2606:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2606:
US-08-956-171E-2606

Query Match 65.0%; Score 13; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGCCACTCCCAT 16
DB 47 TTGCCACTCCCAT 35

RESULT 2
US-08-781-986A-2606/c
Sequence 2606, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781.986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 2606:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2606

Query Match 65.0%; Score 13; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGCCACTCCCAT 16
DB 47 TTGCCACTCCCAT 35

RESULT 3
US-09-262-773-113
Sequence 113, Application US/09262773
Patent No. 6225451
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
FILE REFERENCE: MYRIAD 3
CURRENT APPLICATION NUMBER: US/09/262,773

CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 113
LENGTH: 21
TYPE: DNA
ORGANISM: primer
US-09-262-773-113

Query Match 60.0%; Score 12; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGCCACTCCCA 15
DB 2 TTGCCACTCCCA 13

RESULT 4
US-09-396-196G-64405
Sequence 64405, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64405
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-64405

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATTGCCACTCC 13
DB 8 CATTGCCACTCC 19

RESULT 5
US-09-396-196G-106332
Sequence 106332, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 106332
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-106332

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 7 GCATTGCCACTC 18

RESULT 6

US-09-396-196G-106334
; Sequence 106334, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106333

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 5 GCATTGCCACTC 16

RESULT 7

US-09-396-196G-106334
; Sequence 106334, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106334

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 3 GCATTGCCACTC 14

RESULT 8

US-08-846-012A-8/c
; Sequence 8, Application US/08846012A
; Patent No. 5807740
; GENERAL INFORMATION:
; APPLICANT: AMARAL, M. Catherine.
; APPLICANT: CHEN, Jin-Long
; TITLE OF INVENTION: Regulators of UCP2 Gene Expression
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,012A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-012A-8

Query Match 60.0%; Score 12; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
DB 20 TTGCCACTCCCA 9

RESULT 9

US-09-100-297-8/c
; Sequence 8, Application US/09100297
; Patent No. 5849514
; GENERAL INFORMATION:
; APPLICANT: AMARAL, M. Catherine.
; APPLICANT: CHEN, Jin-Long
; TITLE OF INVENTION: Regulators of UCP2 Gene Expression
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,297

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,012
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-100-297-8

Query Match 60.0%; Score 12; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
DB 20 TTGCCACTCCCA 9

RESULT 10
US-09-052-995-8/c
Sequence 8, Application US/09052995
Patent No. 6183956
GENERAL INFORMATION:
APPLICANT: Sivaraaja, Mohanram
APPLICANT: Strulovici, Beta
APPLICANT: Flores, Osvaldo A.
TITLE OF INVENTION: High Throughput In Vitro Screening Assay
TITLE OF INVENTION: For Transcription Modulators
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,995
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018781-00060005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-052-995-8

Query Match 60.0%; Score 12; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CACTCCCATCTT 19
DB 27 CACTCCCATCTT 16

RESULT 11
US-08-758-306-997
Sequence 997, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PasteSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 997:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-997

Query Match 55.0%; Score 11; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATTGCCACTC 12
DB 6 CATTGCCACTC 16

RESULT 12
US-09-690-185A-5/c
Sequence 5, Application US/09690185A
Patent No. 6471964
GENERAL INFORMATION:

APPLICANT: BIERING, EIRIK
 APPLICANT: KROSSOY, BJORN
 TITLE OF INVENTION: DNA ENCODING STRUCTURAL PROTEIN-1 OF INFECTIOUS SALMON
 TITLE OF INVENTION: ANAEMIA VIRUS AND USES THEREOF
 FILE REFERENCE: BIERING
 CURRENT APPLICATION NUMBER: US/09/690,185A
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: EP99203401.7
 PRIOR FILING DATE: 1999-10-18
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 5
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Infectious salmon anemia virus
 FEATURE:
 NAME/KEY: primer bind
 LOCATION: (1)..(18)
 US-09-690-185A-5

Query Match 55.0%; Score 11; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
 |||||
 Db 15 TGGCACTCCCA 5

RESULT 13
 US-08-853-164C-5/c
 Sequence 5, Application US/08853164C
 Patent No. 6489163
 GENERAL INFORMATION:
 APPLICANT: Roy, Arun K.
 APPLICANT: Chen, Shuo
 TITLE OF INVENTION: RIBOZYME MEDIATED INACTIVATION OF THE ANDROGEN RECEPTOR
 FILE REFERENCE: 4003.001500
 CURRENT APPLICATION NUMBER: US/08/853,164C
 CURRENT FILING DATE: 1997-05-08
 PRIOR APPLICATION NUMBER: 60/016,590
 PRIOR FILING DATE: 1996-05-08
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 5
 LENGTH: 18
 TYPE: DNA
 ORGANISM: ARTIFICIAL SEQUENCE
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(7)
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
 US-08-853-164C-5

Query Match 55.0%; Score 11; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
 |||||
 Db 13 TGGCACTCCCA 3

RESULT 14
 US-09-230-196-46
 Sequence 46, Application US/09230196
 Patent No. 6307035
 GENERAL INFORMATION:
 APPLICANT: Rauscher III, Frank J.
 APPLICANT: Jensen, David E.
 TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and
 TITLE OF INVENTION: Uses Therefor
 NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howson and Howson
 STREET: Spring House Corporate Cntr., PO Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/230,196
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/022,997
 FILING DATE: 02-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/038,109
 FILING DATE: 19-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: WST688BUSA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: other nucleic acid
 US-09-230-196-46

Query Match 55.0%; Score 11; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCAT 17
 |||||
 Db 6 CCACCTCCCAT 16

RESULT 15
 US-09-403-861A-4/c
 Sequence 4, Application US/09403861A
 Patent No. 6833348
 GENERAL INFORMATION:
 APPLICANT: RICCARDI, Carlo
 TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
 DEATH PATHWAYS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 STREET: 624 Ninth Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/403,861A
 FILING DATE: 11-Feb-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP98/02490

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; FILING DATE: 27-APR-1998
; APPLICATION NUMBER: EP 9710703.9
; FILING DATE: 28-APR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: YUN, Allen C.
;   REGISTRATION NUMBER: 37,971
;   REFERENCE/DOCKET NUMBER: RICCADI=1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 20 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..20
;   OTHER INFORMATION: /note= "PCR reverse primer"
;
; US-09-403-861A-4
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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```

Query Match      55.0%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 TGCCATGCCCA 15
Db      18 TGCCATGCCCA 8

```

```

RESULT 16
US-09-396-196G-26004
; Sequence 26004, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Lockhart
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 26004
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
;
US-09-396-196G-26004

```

```

Query Match      55.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 GCATTGCCCACT 11
Db      15 GCATTGCCCACT 25

```

```

RESULT 17
US-09-396-196G-26005
; Sequence 26005, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack
;
US-09-396-196G-26005

```

```

; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 26005
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
;
US-09-396-196G-26005

```

```

Query Match      55.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GCATTGCCCACT 11
Db      9 GCATTGCCCACT 19

```

```

RESULT 18
US-09-396-196G-72679
; Sequence 72679, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 72679
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
;
US-09-396-196G-72679

```

```

Query Match      55.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GCATTGCCCACT 11
Db      13 GCATTGCCCACT 23

```

```

RESULT 19
US-09-396-196G-72680
; Sequence 72680, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;
US-09-396-196G-72680

```

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 72680
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-72680

Query Match
 Best Local Similarity 100.0%; Score 11; DB 4; Length 25;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCCACT 11
 DB 1 GCATGCCACT 11

RESULT 20
 US-09-396-196G-91273
 Sequence 91273, Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Miltmann
 APPLICANT: David Mack
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 91273
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-91273

Query Match
 Best Local Similarity 100.0%; Score 11; DB 4; Length 25;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCCACT 11
 DB 5 GCATGCCACT 15

RESULT 21
 US-07-834-539A-24/c
 Sequence 24, Application US/07834539A
 GENERAL INFORMATION:
 APPLICANT: Lomborg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/834,539A
 FILING DATE: 1992-02-05
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,1223
 REFERENCE/DOCKET NUMBER: 14643-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-543-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-07-834-539A-24

Query Match
 Best Local Similarity 100.0%; Score 11; DB 1; Length 42;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
 DB 11 CACTCCCATTC 1

RESULT 22
 US-08-053-131-32/c
 Sequence 32, Application US/08053131
 Patent No. 5661016
 GENERAL INFORMATION:
 APPLICANT: Lomborg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 200
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/053,131
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,1223
 REFERENCE/DOCKET NUMBER: 14643-9-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)
US-08-053-131-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 23

US-08-645-641-32/c
Sequence 32, Application US/08645641
Patent No. 5719032

GENERAL INFORMATION:

APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-MAY-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)
US-08-645-641-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 24

US-07-853-408B-32/c
Sequence 32, Application US/07853408B
Patent No. 5789650

GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-096-762-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 26
US-08-800-353-24/c
Sequence 24, Application US/0800353
Patent No. 5874299
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539
FILING DATE: 1992-02-05
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-800-353-24

Query Match 55.0%; Score 11; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 27
US-08-308-865-32/c
Sequence 32, Application US/0830865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-308-865-32

Query Match 55.0%; Score 11; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 28
US-09-042-353-200/c
Sequence 200, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
NUMBER OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA
US-09-042-353-200

Query Match 55.0%; Score 11; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 29
US-08-758-417A-48/c
Sequence 48, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-758-417A-48

Query Match 55.0%; Score 11; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 30
PCT-US92-06185-24/c
Sequence 24, Application PC/TUS9206185
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 19910828
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
REFERENCE/DOCKET NUMBER: 14643-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US92-06185-24

Query Match 55.0%; Score 11; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATTC 18

Db 11 CACTCCCATTC 1

RESULT 31
PCT-US92-10983-32/c
Sequence 32, Application PC/TUS9210983
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10983
FILING DATE: 19921217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
PCT-US92-10983-32

Query Match 55.0%; Score 11; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 32
US-08-441-887A-59/c
Sequence 59, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbard, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

```

/ STREET: Two Embarcadero Center, 8th Floor
/ City: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/441,887A
/ FILING DATE: 16-MAY-1995
/ CLASSIFICATION: 435
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/082,937
/ FILING DATE: 25-JUN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Liebeschuetz, Joseph O.
/ REGISTRATION NUMBER: 37,505
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-326-2400
/ TELEFAX: 650-326-2422
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (probe)
US-08-441-887A-59

```

```

Query Match
Best Local Similarity 50.0%; Score 10; DB 2; Length 12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCAT 16
Db 12 CCACTCCCAT 3

```

```

RESULT 33
US-09-081-646-147/c
/ Sequence 147, Application US/09081646
/ Patent No. 6333152
/ GENERAL INFORMATION:
/ APPLICANT: Kinzler, Kenneth
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Zhang, Lin
/ APPLICANT: Zhou, Wei
/ TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
/ FILE REFERENCE: 01107.74664
/ CURRENT APPLICATION NUMBER: US/09/081,646
/ EARLIER FILING DATE: 1998-05-20
/ EARLIER FILING DATE: 1997-05-21
/ NUMBER OF SEQ ID NOS: 871
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 147
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-081-646-147

```

```

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 CCACTCCCAT 16
Db 11 CCACTCCCAT 2

```

```

RESULT 34
US-09-081-646-830/c
/ Sequence 830, Application US/09081646
/ Patent No. 6333152
/ GENERAL INFORMATION:
/ APPLICANT: Kinzler, Kenneth
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Zhang, Lin
/ APPLICANT: Zhou, Wei
/ TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
/ FILE REFERENCE: 01107.74664
/ CURRENT APPLICATION NUMBER: US/09/081,646
/ EARLIER FILING DATE: 1998-05-20
/ EARLIER FILING DATE: 1997-05-21
/ NUMBER OF SEQ ID NOS: 871
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 830
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-081-646-830

```

```

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCAT 16
Db 11 CCACTCCCAT 2

```

```

RESULT 35
US-09-213-719-54
/ Sequence 54, Application US/092137198
/ Patent No. 6150163
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ APPLICANT: Lex M. Cowsett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION
/ FILE REFERENCE: RTS-0006
/ CURRENT APPLICATION NUMBER: US/09/213,7198
/ EARLIER FILING DATE: 1998-12-17
/ NUMBER OF SEQ ID NOS: 91
/ SEQ ID NO 54
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-213-719-54

```

```

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATTGCCACT 11
Db 8 CATTGCCACT 17

```

```

RESULT 36
US-09-422-978-8213/c
/ Sequence 8213, Application US/09422978
/ Patent No. 6537751
/ GENERAL INFORMATION:

```

```

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8213
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-14446 for SEQ 348, in compleme
US-09-422-978-8213

Query Match          50.0%; Score 10; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATGCCAC 10
DB      10 GCATGCCAC 1

RESULT 37
US-09-155-885A-267/C
; Sequence 267, Application US/09155885A
; Patent No. 6709812
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 9687053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 267:
US-09-155-885A-267

Query Match          50.0%; Score 10; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCACTCCCAT 16
DB      11 CCACTCCCAT 2

RESULT 38
US-09-422-978-5302
; Sequence 5302, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5302
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-23334 for SEQ 1368,
US-09-422-978-5302

Query Match          50.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCCATCTT 20
DB      4 TCCCATCTT 13

RESULT 39
US-09-696-791-3881
; Sequence 3881, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3881
; LENGTH: 19

```

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3881

Query Match 50.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCC 13
Db 9 TTGCCACTCC 18

RESULT 40
US-09-696-791-3882
Sequence 3882, Application US/09696791
Patent No. 6770633
GENERAL INFORMATION:

APPLICANT: Robbins, Joan M.
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3882
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3882

Query Match 50.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCC 13
Db 2 TTGCCACTCC 11

RESULT 41
US-10-141-021-15/c
Sequence 15, Application US/10141021
Patent No. PPI4777
GENERAL INFORMATION:

APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 4"
FILE REFERENCE: 30034-93461
CURRENT APPLICATION NUMBER: US/10/141,021
CURRENT FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-021-15

Query Match 50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCCACTC 12
Db 11 ATTGCCACTC 2

RESULT 42
US-10-141-103-15/c
Sequence 15, Application US/10141103
Patent No. PPI4829
GENERAL INFORMATION:

APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 5"
FILE REFERENCE: 30034-93462
CURRENT APPLICATION NUMBER: US/10/141,103
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-103-15

Query Match 50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCCACTC 12
Db 11 ATTGCCACTC 2

RESULT 43
US-10-141-063-15/c
Sequence 15, Application US/10141063
Patent No. PPI4839
GENERAL INFORMATION:

APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 10"
FILE REFERENCE: 30034-93467
CURRENT APPLICATION NUMBER: US/10/141,063
CURRENT FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-063-15

Query Match 50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCCACTC 12
Db 11 ATTGCCACTC 2

RESULT 44
US-10-141-094-15/c
Sequence 15, Application US/10141094
Patent No. PPI4978
GENERAL INFORMATION:

APPLICANT: BEINEKE, WALTER F.
TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 6"
FILE REFERENCE: 30034-93463
CURRENT APPLICATION NUMBER: US/10/141,094
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-094-15

```

```

Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 ATTGCCACTC 12
        |||||
Db      11 ATTGCCACTC 2

```

```

RESULT 45
US-10-141-060-15/c
; Sequence 15, Application US/10141060
; Patent No. PP15079
; GENERAL INFORMATION:
; APPLICANT: BEINKE, WALTER F.
; TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINKE 1"
; FILE REFERENCE: 30034-92642
; CURRENT APPLICATION NUMBER: US/10/141,060
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-060-15

```

```

Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 ATTGCCACTC 12
        |||||
Db      11 ATTGCCACTC 2

```

Search completed: September 14, 2005, 11:45:54
Job time : 124 secs

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 10:15:01 ; Search time 482 Seconds
(without alignments)
272.500 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcattgccacccattctt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

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Total number of hits satisfying chosen parameters: 8541662

Minimum DB seq length: 8
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Published Applications NA:*

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- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
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- 21: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 22: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 23: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 24: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 25: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 26: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 21 US-10-643-801-35	Sequence 35, App1
2	20	100.0	20 21 US-10-643-801-157	Sequence 157, App1
3	15	75.0	20 21 US-10-643-801-36	Sequence 36, App1
4	15	75.0	20 21 US-10-643-801-158	Sequence 158, App1
5	15	75.0	25 21 US-10-719-900-415646	Sequence 415646,
6	13	65.0	25 21 US-10-719-900-136702	Sequence 136702,
7	13	65.0	25 21 US-10-719-900-840616	Sequence 840616,

C	8	13	65.0	25	22	US-10-843-527-86272	Sequence 86272, A
	9	13	65.0	25	22	US-10-843-527-151905	Sequence 151905,
	10	13	65.0	25	22	US-10-719-956-650147	Sequence 650147,
	11	13	65.0	54	8	US-08-781-9864-2606	Sequence 2606, Ap
	12	13	65.0	54	18	US-10-329-624-2606	Sequence 2606, Ap
	13	13	65.0	60	10	US-09-908-975-18015	Sequence 18015, A
	14	12	60.0	12	20	US-10-257-017B-267933	Sequence 267933,
	15	12	60.0	12	20	US-10-257-017B-269218	Sequence 269218,
	16	12	60.0	12	20	US-10-303-633-73	Sequence 73, App1
	17	12	60.0	20	19	US-10-303-633-74	Sequence 74, App1
	18	12	60.0	20	19	US-10-303-633-192	Sequence 192, App
	19	12	60.0	20	22	US-10-257-158A-5395	Sequence 5395, Ap
	20	12	60.0	24	22	US-10-257-158A-762	Sequence 762, App
	21	12	60.0	25	21	US-10-719-900-198562	Sequence 198562,
	22	12	60.0	25	21	US-10-719-900-264711	Sequence 264711,
	23	12	60.0	25	21	US-10-719-900-305113	Sequence 305113,
	24	12	60.0	25	21	US-10-719-900-903551	Sequence 903551,
	25	12	60.0	25	21	US-10-719-900-964504	Sequence 964504,
	26	12	60.0	25	21	US-10-719-900-974937	Sequence 974937,
	27	12	60.0	25	21	US-10-809-189-64405	Sequence 64405, A
	28	12	60.0	25	21	US-10-809-189-106332	Sequence 106332,
	29	12	60.0	25	21	US-10-809-189-106333	Sequence 106333,
	30	12	60.0	25	21	US-10-809-189-106334	Sequence 106334,
	31	12	60.0	25	22	US-10-843-527-19523	Sequence 19523, A
	32	12	60.0	25	22	US-10-843-527-20511	Sequence 20511, A
	33	12	60.0	25	22	US-10-843-527-216202	Sequence 216202,
	34	12	60.0	25	22	US-10-843-527-217190	Sequence 217190,
	35	12	60.0	25	22	US-10-719-956-143538	Sequence 143538,
	36	12	60.0	25	22	US-10-719-956-16560	Sequence 16560,
	37	12	60.0	25	22	US-10-719-956-329530	Sequence 329530,
	38	12	60.0	25	22	US-10-719-956-329531	Sequence 329531,
	39	12	60.0	25	22	US-10-719-956-693459	Sequence 693459,
	40	12	60.0	26	16	US-10-025-806-257	Sequence 257, App
	41	12	60.0	51	20	US-10-813-633-4478	Sequence 478, App
	42	12	60.0	60	10	US-09-908-975-15069	Sequence 15069, A
	43	12	60.0	60	10	US-09-908-975-117268	Sequence 117268, A
	44	11	55.0	13	20	US-10-257-017B-14061	Sequence 14061, A
	45	11	55.0	13	20	US-10-257-017B-14062	Sequence 14062, A

ALIGNMENTS

RESULT 1
US-10-643-801-35
Sequence 35, Application US/10643801
Publication No. US20050043524A1
GENERAL INFORMATION:
APPLICANT: Sanjay Bhano
TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
FILE REFERENCE: RTS-0678US
CURRENT APPLICATION NUMBER: US/10/643,801
CURRENT FILING DATE: 2003-08-18
NUMBER OF SEQ ID NOS: 230
SEQ ID NO 35
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-35

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCCATTCTT 20
DB 1 GCATTGCCATCCATTCTT 20

RESULT 2

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US-10-643-801-157/c
; Sequence 157, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-067805
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-643-801-157
```

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Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCATTGCCACTCCCTT 20
Db 20 GCATTGCCACTCCCTT 1
```

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RESULT 3
US-10-643-801-36
; Sequence 36, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-067805
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-36
```

```
Query Match
Best Local Similarity 75.0%; Score 15; DB 21; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCATTGCCACTCCCA 15
Db 6 GCATTGCCACTCCCA 20
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RESULT 4
US-10-643-801-158/c
; Sequence 158, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-067805
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
```

```
US-10-643-801-158
```

```
Query Match
Best Local Similarity 75.0%; Score 15; DB 21; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCATTGCCACTCCCA 15
Db 15 GCATTGCCACTCCCA 1
```

```
RESULT 5
US-10-719-900-415646
; Sequence 415646, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 415646
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-415646
```

```
Query Match
Best Local Similarity 75.0%; Score 15; DB 21; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 CATTGCCACTCCCAT 16
Db 4 CATTGCCACTCCCAT 18
```

```
RESULT 6
US-10-719-900-136702/c
; Sequence 136702, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 136702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-136702
```

```
Query Match
Best Local Similarity 65.0%; Score 13; DB 21; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 5 TGCCACTCCCAT 17
Db 23 TGCCACTCCCAT 11
```

```
RESULT 7
US-10-719-900-840616
; Sequence 840616, Application US/10719900
; Publication No. US20050026164A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 840616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-840616

Query Match          65.0%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTCC 13
DB      6 GCATTGCCACTCC 18

RESULT 8
US-10-843-527-86272/c
; Sequence 86272, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
; US-10-843-527-86272

Query Match          65.0%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CACTCCCATCTT 20
DB      18 CACTCCCATCTT 6

RESULT 9
US-10-843-527-151905
; Sequence 151905, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151905
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: SARS Virus
; US-10-843-527-151905

Query Match          65.0%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CACTCCCATCTT 20
DB      8 CACTCCCATCTT 20

RESULT 10
US-10-719-956-650147
; Sequence 650147, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 659466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 650147
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-650147

Query Match          65.0%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGCCACTCCCAT 17
DB      10 TGCCACTCCCAT 22

RESULT 11
US-08-781-986A-2606/c
; Sequence 2606, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2606:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2606

Query Match 65.0%; Score 13; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
DB 47 TTGCCACTCCCAT 35

RESULT 12
US-10-329-624-2606/c
Sequence 2606, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1324
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2606:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2606:
US-10-329-624-2606

Query Match 65.0%; Score 13; DB 18; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
DB 47 TTGCCACTCCCAT 35

RESULT 13
US-09-908-975-18015
Sequence 18015, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: MASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simcha
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC-
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18015
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-18015

Query Match 65.0%; Score 13; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
DB 4 TTGCCACTCCCAT 16

RESULT 14
US-10-257-017B-267933
Sequence 267933, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 267933
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00000710
US-10-257-017B-267933

Query Match 60.0%; Score 12; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATTC 18
DB 1 CCACTCCCATTC 12

```
RESULT 15
US-10-257-017B-269218/C
; Sequence 269218, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Beclin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269218
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00001665
US-10-257-017B-269218

Query Match          60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CACTCCCATCTCT 19
        |||||
Db      12 CACTCCCATCTCT 1

RESULT 16
US-10-303-635-73
; Sequence 73, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-73

Query Match          60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTC 12
        |||||
Db      6 GCATTGCCACTC 17

RESULT 17
US-10-303-635-74
; Sequence 74, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
```

```
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-74

Query Match          60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTC 12
        |||||
Db      9 GCATTGCCACTC 20

RESULT 18
US-10-303-635-192/C
; Sequence 192, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 192
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-303-635-192

Query Match          60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTC 12
        |||||
Db      15 GCATTGCCACTC 4

RESULT 19
US-10-257-158A-5395/C
; Sequence 5395, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Zilivl, Monib
; APPLICANT: Gerry, Norman P.
; APPLICANT: Favis, Reyna
; APPLICANT: Kisman, Richard
; TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC A
; FILE REFERENCE: 19603/2834
; CURRENT APPLICATION NUMBER: US/10/257,158A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/US01/10958
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/197,271
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 9544
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5395
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
US-10-257-158A-5395
```

Query Match 60.0%; Score 12; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTC 12
Db 15 GCATTGCCACTC 4

RESULT 20

US-10-257-158A-762/C
; Sequence 762, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Zivri, Monib
; APPLICANT: Getty, Norman P.
; APPLICANT: Favis, Reyna
; APPLICANT: Kilman, Richard
; TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC AC
; FILE REFERENCE: 19603/2834
; CURRENT APPLICATION NUMBER: US/10/257,158A
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/US01/10958
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/197,271
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 9544
; SOFTWARE: Patent version 3.1
; SEQ ID NO 762
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
US-10-257-158A-762

Query Match

Best Local Similarity 60.0%; Score 12; DB 22; Length 24;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTC 12
Db 19 GCATTGCCACTC 8

RESULT 21

US-10-719-900-198562/C
; Sequence 198562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-198562

Query Match

Best Local Similarity 60.0%; Score 12; DB 21; Length 25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCCACTCCC 14

Db 13 ATTGCCACTCCC 2

RESULT 22

US-10-719-900-264711
; Sequence 264711, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 264711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-264711

Query Match

Best Local Similarity 60.0%; Score 12; DB 21; Length 25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCCACTCCCAT 17
Db 4 GCCACTCCCAT 15

RESULT 23

US-10-719-900-305113
; Sequence 305113, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 305113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-305113

Query Match

Best Local Similarity 60.0%; Score 12; DB 21; Length 25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACTGCCACTCT 20
Db 11 ACTGCCACTCT 22

RESULT 24

US-10-719-900-903551
; Sequence 903551, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

;; PRIOR FILING DATE: 2002 11 20
;; NUMBER OF SEQ ID NOS: 982914
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 903551
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-719-900-903551

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATCT 19
Db 12 CACTCCCATCT 23

RESULT 25
US-10-719-900-964504/c
; Sequence 964504, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 964504
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-964504

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCTC 12
Db 21 GCATTGCCATCTC 10

RESULT 26
US-10-719-900-974937
; Sequence 974937, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 974937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-974937

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCTC 12
Db 12 GCATTGCCATCTC 12

Db 5 GCATTGCCATCTC 16

RESULT 27
US-10-809-189-64405
; Sequence 64405, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-64405

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATTGCCATCTCC 13
Db 8 CATTGCCATCTCC 19

RESULT 28
US-10-809-189-106332
; Sequence 106332, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-106332

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCTC 12
Db 7 GCATTGCCATCTC 18

RESULT 29
US-10-809-189-106333

```

; Sequence 106333, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-106333

```

```

Query Match      60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCATTGCCACTC 12
Db      5 GCATTGCCACTC 16

```

```

RESULT 30
US-10-809-189-106334
; Sequence 106334, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-106334

```

```

Query Match      60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCATTGCCACTC 12
Db      3 GCATTGCCACTC 14

```

```

RESULT 31
US-10-843-527-19523
; Sequence 19523, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
US-10-843-527-19523

```

```

; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 19523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-19523

```

```

Query Match      60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 CACTCCCATCTT 19
Db      13 CACTCCCATCTT 24

```

```

RESULT 32
US-10-843-527-20511
; Sequence 20511, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-20511

```

```

Query Match      60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      9 ACTCCCATCTT 20
Db      2 ACTCCCATCTT 13

```

```

RESULT 33
US-10-843-527-216202/c
; Sequence 216202, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-216202

```

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCACTTCTT 20
DB 24 ACTCCACTTCTT 13

RESULT 34
US-10-843-527-217190/c
; Sequence 217190, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; FILE REFERENCE: 3602.1
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 217190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-217190

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCACTTCTT 19
DB 13 CACTCCACTTCTT 2

RESULT 35
US-10-719-956-143538/c
; Sequence 143538, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 143538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-143538

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTTCCCAT 16
DB 22 TGCCACTTCCCAT 11

RESULT 36
US-10-719-956-166560/c
; Sequence 166560, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 166560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-166560

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTTCCCAT 16
DB 17 TGCCACTTCCCAT 6

RESULT 37
US-10-719-956-329530
; Sequence 329530, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329530
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-329530

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCACTTCTT 20
DB 14 ACTCCACTTCTT 25

RESULT 38
US-10-719-956-329531
; Sequence 329531, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-329531

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCATCTCT 20
|||||
Db 14 ACTCCATCTCT 25

RESULT 39
US-10-719-956-693459
; Sequence 693459, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 693459
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-693459

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTGCCA 15
|||||
Db 2 TTGCCACTGCCA 13

RESULT 40
US-10-025-806-257
; Sequence 257, Application US/10025806
; Publication No. US20030198955A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Ballinger, Robert
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Coleman, Steven
; APPLICANT: Spytek, Kimberly
; APPLICANT: Caaman, Stacie
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Sciore, Paul
; APPLICANT: Smithson, Glenda
; APPLICANT: Peyman, John
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Vernet, Corine
; APPLICANT: Shenoy, Suresh
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Tchernev, Velizar
; APPLICANT: Anderson, David
; APPLICANT: Gusev, Vladimir
; APPLICANT: Malyankar, Uriel
; APPLICANT: Zhong, Hailong
; APPLICANT: Ellerman, Karen
; APPLICANT: Wolenc, Adam
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-224 AB
; CURRENT APPLICATION NUMBER: US/10/025,806
; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/256,635
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/259,743
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/239,327
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/261,498
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/263,689
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/276,464
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/271,021
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/275,946
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/278,150
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/285,718
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/312,902
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/257,876
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/260,718
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/284,591
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TagMan PCR
US-10-025-806-257

Query Match 60.0%; Score 12; DB 16; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTGCCA 15
|||||
Db 5 TTGCCACTGCCA 16

RESULT 41
US-10-813-638-478/c
; Sequence 478, Application US/10813638
; Publication No. US20040235026A1
; GENERAL INFORMATION:
; APPLICANT: Shinkels, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND M
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/10/813,638
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 478
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism

```
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg44005525
US-10-813-638-478
```

```
Query Match          60.0%; Score 12; DB 20; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCATTGCCACTC 12
         |||||
Db       27 GCATTGCCACTC 16
```

```
RESULT 42
US-09-908-975-15069/c
; Sequence 15069, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15069
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-15069
```

```
Query Match          60.0%; Score 12; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 ACTCCCATCTCT 20
         |||||
Db       17 ACTCCCATCTCT 6
```

```
RESULT 43
US-09-908-975-17268
; Sequence 17268, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17268
; LENGTH: 60
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-17268
```

```
Query Match          60.0%; Score 12; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCATTGCCACTC 12
         |||||
Db       44 GCATTGCCACTC 55
```

```
RESULT 44
US-10-257-017B-14061/c
; Sequence 14061, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14061
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003215
US-10-257-017B-14061
```

```
Query Match          55.0%; Score 11; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 ACTCCCATCTCT 19
         |||||
Db       13 ACTCCCATCTCT 3
```

```
RESULT 45
US-10-257-017B-14062
; Sequence 14062, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14062
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003215
US-10-257-017B-14062
```

```
Query Match          55.0%; Score 11; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 9 ACTCCCATCT 19
Db 1 ACTCCCATCT 11

Search completed: September 14, 2005, 11:54:03
Job time : 484 secs
